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OM protein - protein search, using sw model

Run on: February 12, 2003, 11:08:41 ; Search time 14 Seconds

(without alignments)
1128.749 Million cell updates/sec

Title: US-09-623-035-2

Perfect score: 381

Sequence: 1 MTVPSPVPALPLGLGLPR.....HTCFLLTGLGLVWGLLT 381

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 112892 seqs, 41476328 residues

Word size : 0 112892

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	301	79.0	381	DAF_HUMAN	P08174 homo sapien
2	85	22.3	340	DAF_PONPY	P49457 pongo pygma
3	13	3.4	507	DAF_CAVPO	Q60401 cavia porce
4	10	2.6	390	DAF1_MOUSE	Q61475 mus musculu
5	10	2.6	407	DAF2_MOUSE	Q61476 mus musculu
6	9	2.4	345	APOR_HUMAN	P02749 homo sapien
7	8	2.1	307	TAL_PSEAE	Q91047 pseudomonas
8	8	2.1	322	ASPE_DETRA	Q91893 delnoccocus
9	8	2.1	503	TGRI_HUMAN	P36897 homo sapien
10	8	2.1	522	PME_PRUPE	Q43062 prunus pers
11	8	2.1	555	UL25_HSV62	P52537 human herpe
12	8	2.1	558	C4BP_RAF	Q63514 rattus norv
13	8	2.1	89	RS15_PSEPU	O87791 pseudomonas
14	7	1.8	119	B2MG_CEBAL	O77826 cebus albid
15	7	1.8	119	B2MG_CHISA	P37652 chiropteres
16	7	1.8	143	YIBN_ECOLI	O37688 escherichia
17	7	1.8	156	RNP_HUMAN	P07998 homo sapien
18	7	1.8	204	CPCE_SYNP7	Q44116 synechococc
19	7	1.8	219	YGBH_SALTU	P18951 salmonella
20	7	1.8	230	CLD2_CANFA	Q95KM6 canis fami
21	7	1.8	230	CLD2_HUMAN	P57739 homo sapien
22	7	1.8	272	MSA2_PLAF7	P50498 plasmodium
23	7	1.8	275	Y0JG_BACSU	P54544 bacillus su
24	7	1.8	284	SMX5_SCHMA	Q26604 schistosoma
25	7	1.8	286	SSRA_CANFA	P16967 canis fami
26	7	1.8	286	SSRA_HUMAN	P43307 homo sapien
27	7	1.8	286	SSRA_RABIT	P53815 oryctolagus
28	7	1.8	291	RGR_BOVIN	P47803 bos taurus
29	7	1.8	291	RGR_HUMAN	P47804 homo sapien
30	7	1.8	303	CAT2_HUMAN	O9ubt2 homo sapien
31	7	1.8	341	MOZ2_MOUSE	O06138 mus musculu
32	7	1.8	355	CHLI_NEPOL	O9t108 nephrolepis
33	7	1.8	365	CYB_ASCSU	P24878 ascaris suu

34	7	1.8	373	1	YC08_KLEPN	Q48454 klebsiella
35	7	1.8	375	1	GDF8_CHICK	O42220 gallus gall
36	7	1.8	375	1	GDF8_MERGA	O42221 meleagris g
37	7	1.8	377	1	MLC1_HUMAN	O15049 homo sapien
38	7	1.8	379	1	CYB_EQUUS	P92487 equus asinu
39	7	1.8	381	1	CYB_ANTNA	Q3800 antechinus
40	7	1.8	381	1	CYB_DASHA	Q34321 dasypus ha
41	7	1.8	381	1	CYB_NEOLO	Q35157 neophascoga
42	7	1.8	381	1	CYB_PHAEL	Q35409 phascogale
43	7	1.8	381	1	CYB_PHARA	Q35673 phascogale
44	7	1.8	381	1	CYB_PSEMO	Q35695 pseudantech
45	7	1.8	381	1	CYB_SMICR	Q35810 smilthopsis

ALIGNMENTS

RESULT 1

DAF_HUMAN STANDARD; PRT; 381 AA.

AC P08174; P06679; P78361;

DT 01-AUG-1988 (Rel. 08, Created)

DT 01-FEB-1996 (Rel. 33, Last sequence update)

DT 15-JUN-2002 (Rel. 41, Last annotation update)

DE Complement decay-accelerating factor precursor (CD55 antigen).

GN DAF OR CR OR CD55.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RN SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).

RX MEDLINE=87115845; PubMed=2433596;

RA Carras I.W., Davitz M.A., Rhee L., Wedgell G., Martin D.W. Jr.,

RA Nussenzweig V.;

RT "Cloning of decay-accelerating factor suggests novel use of splicing

RT to generate two proteins.";

RL Nature 325:545-549(1987).

RN [2]

RN SEQUENCE FROM N.A.

RC TISSUE=Cervix;

RA Strausberg R.;

RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.

RN [3]

RN SEQUENCE OF 6-381 FROM N.A. (ISOFORM 2).

RX MEDLINE=87175602; PubMed=2436222.

RA Medof M.E., Lublin D.M., Holers V.M., Ayers D.J., Getty R.R.,

RA Leykam J.F., Atkinson J.P., Tykocinski M.L.;

RT "Cloning and characterization of cDNAs encoding the complete sequence

RT of decay-accelerating factor of human complement.";

RL Proc. Natl. Acad. Sci. U.S.A. 84:2007-2011(1987).

RN [4]

RN SEQUENCE OF 35-381 FROM N.A. (ISOFORM 2).

RC TISSUE=Hipocampus;

RA Kumar V.B., Hyung C., Nakra R., Walters M., Sasser T., Bernardo A.;

RT "Decay-acceleration factor (DAF; CD 55) in the brain of Alzheimer's

RT disease patients.";

RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.

RN [5]

RN SEQUENCE OF 1-100 FROM N.A.

RX MEDLINE=91271256; PubMed=1711208;

RA Ewlonu U.K., Ravi L., Medof M.E.;

RT "Characterization of the decay-accelerating factor gene promoter

RT region.";

RL Proc. Natl. Acad. Sci. U.S.A. 88:4675-4679(1991).

RN [6]

RN SEQUENCE OF 35-46.

RC TISSUE=Urine;

RA MEDLINE=91291869; PubMed=1712233;

RX Nakano Y., Sugita Y., Ishikawa Y., Choi N.-H., Tobe T., Tomita M.;

RT "Isolation of two forms of decay-accelerating factor (DAF) from human

RT urine.";

RL Biochim. Biophys. Acta 1074:326-330(1991).

CC [7]
CC GPI-ANCHOR.
CC MEDLINE-91093238; PubMed-1824699;
CC Moran P., Raab H., Kohr W.J., Carras I.W.;
CC "Glycophospholipid membrane anchor attachment. Molecular analysis of
CC the cleavage/attachment site.";
CC J. Biol. Chem. 266:1250-1257(1991).
CC (8)
CC DISULFIDE BONDS IN SUSHI DOMAINS.
CC MEDLINE-92305034; PubMed-1377029;
CC Nakano Y., Sumida K., Kikuta N., Mura N.-H., Tobe T., Tomita M.;
CC Complete determination of disulfide bonds localized within the short
CC consensus repeat units of decay accelerating factor (CD55 antigen).";
CC Biochim. Biophys. Acta 1116:235-240(1992).
CC (9)
CC FUNCTION AS A ECHOVIRUS RECEPTOR.
CC MEDLINE-95045399; PubMed-7535274;
CC Ward T., Pipkin P.A., Clarkson N.A., Stone D.M., Minor P.D.,
CC Almond J.W.;
CC "Decay-accelerating factor CD55 is identified as the receptor for
CC echovirus 7 using CELICS, a rapid immuno-focal cloning method.";
CC EMBO J. 13:5070-5074(1994).
CC (10)
CC VARIANT BLOOD GROUP DR(A-).
CC MEDLINE-94325573; PubMed-7519480;
CC Lublin D.M., Mallinson G., Poole J., Reid M.E., Thompson E.S.,
CC Ferdman B.R., Telen M.J., Anstee D.J., Tanner M.J.A.;
CC "Molecular basis of reduced or absent expression of
CC decay-accelerating factor in Cromer blood group phenotypes.";
CC Blood 84:1276-1282(1994).
CC -1- FUNCTION: THIS PROTEIN RECOGNIZES C4B AND C3B FRAGMENTS THAT
CC CONDENSE WITH CELL-SURFACE HYDROXYL OR AMINO GROUPS WHEN NASCENT
CC C4B AND C3B ARE LOCALLY GENERATED DURING C4 AND C3 ACTIVATION.
CC INTERACTION OF DAF WITH CELL-ASSOCIATED C4B AND C3B POLYPEPTIDES
CC INTERFERES WITH THEIR ABILITY TO CATALYZE THE CONVERSION OF C2 AND
CC FACTOR B TO ENZYMATICALLY ACTIVE C2A AND BB AND THEREBY PREVENTS
CC THE FORMATION OF C4B2A AND C3BBB, THE AMPLIFICATION CONVERTASES OF
CC THE COMPLEMENT CASCADE.
CC -1- FUNCTION: ALSO ACTS AS THE RECEPTOR FOR ECHOVIRUS 7 AND RELATED
CC VIRUSES (ECHOVIRUSES 13, 21, 29 AND 33).
CC -1- SUBUNIT: MONOMER (MAJOR FORM) AND NON-DISULFIDE-LINKED, COVALENT
CC HOMODIMER (MINOR FORM).
CC -1- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor.
CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS: 1/DAF-1 AND 2/DAF-2 (SHOWN
CC HERE); ARE PRODUCED BY ALTERNATIVE SPLICING.
CC -1- TISSUE SPECIFICITY: EXPRESSED ON THE PLASMA MEMBRANES OF ALL CELL
CC TYPES THAT ARE IN INTIMATE CONTACT WITH PLASMA MEMBRANES OF ALL CELL
CC LINES. IT IS ALSO FOUND ON THE SURFACES OF EPITHELIAL CELLS
CC Lining EXTRACELLULAR COMPARTMENTS, AND VARIANTS OF THE MOLECULE
CC ARE PRESENT IN BODY FLUIDS AND IN EXTRACELLULAR MATRIX.
CC -1- DOMAIN: THE FIRST SUSHI DOMAIN (SCR1) IS NOT NECESSARY FOR
CC FUNCTION. SCR2 AND SCR4 PROVIDE THE PROPER CONFORMATION FOR THE
CC ACTIVE SITE ON SCR3 (BY SIMILARITY).
CC -1- PTM: THE SER/THR-RICH DOMAIN IS HEAVILY O-GLYCOSYLATED.
CC -1- POLYMORPHISM: DAF IS RESPONSIBLE FOR THE CROMER BLOOD GROUP
CC SYSTEM. IT CONSISTS OF AT LEAST SEVEN HIGH-INCIDENCE (CRA),
CC TC(A), DR(A), ES(A), MES(B), UMC, AND IFC) AND LOW-INCIDENCE
CC (TC(B), TC(C), AND MES(A)) ANTIGENS THAT RESIDE ON DAF. IN THE
CC CROMER PHENOTYPES DR(A-) AND INAB THERE IS REDUCED OR ABSENT
CC EXPRESSION OF DAF, RESPECTIVELY. IN THE CASE OF THE DR(A-)
CC PHENOTYPE, A SINGLE NUCLEOTIDE SUBSTITUTION WITHIN EXON 5 ACCOUNTS
CC FOR TWO CHANGES: A SIMPLE AMINO ACID SUBSTITUTION THAT IS THE
CC BASIS OF THE ANTIGENIC VARIATION, AND AN ALTERNATIVE SPLICING
CC EVENT THAT UNDERLIES THE DECREASED EXPRESSION OF DAF IN THIS
CC PHENOTYPE.
CC -1- SIMILARITY: CONTAINS 4 SUSHI (SCR) DOMAINS.
CC -1- SIMILARITY: BELONGS TO THE RECEPTORS OF COMPLEMENT ACTIVATION
CC (RCA) FAMILY.
CC (RCA) FAMILY.
CC -1- DATABASE: NAME-PROW: NOTE=CD guide CD55 entry;
CC WWW="http://www.ncbi.nlm.nih.gov/prow/cd/cd55.htm".
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CC or send an email to license@sib.ch).
CC -----
CC DR EMBL: M31516; AAA52169.1; -
CC DR EMBL: M30142; AAA52168.1; -
CC DR EMBL: BC001288; AAH01288.1; -
CC DR EMBL: M15799; AAA52167.1; -
CC DR EMBL: U08576; AAB48622.1; -
CC DR EMBL: M64653; AAA52170.1; -
CC DR EMBL: M64356; AAA52170.1; JOINED.
CC DR EMBL: S72858; AAC60633.1; -
CC DR PIR: B26359; B26359.
CC DR PIR: A26359; A26359.
CC DR PIR: S16187; S16187.
CC DR PIR: A39101; A39101.
CC DR PIR: S23138; S23138.
CC DR HSSP: P08603; IHCC.
CC DR Genew: HGNC:2665; DAF.
CC DR MIM: 125240; -
CC DR InterPro: IPR000436; Sushi_SCR_CCP.
CC DR Pfam: PF00084; sushi; 8.
CC DR SMART: SM00032; CCP; 4.
CC KW Complement pathway; Plasma; Glycoprotein; Membrane; Repeat;
CC Alternative splicing; GPI-anchor; Signal; Polymorphism;
CC Blood group antigen.
CC FT SIGNAL 1 34
CC FT CHAIN 35 353
CC FT PROPEP 354 381
CC FT DOMAIN 35 35
CC FT DOMAIN 97 159
CC FT DOMAIN 162 221
CC FT DOMAIN 224 284
CC FT DOMAIN 287 356
CC FT DISULFID 36 81
CC FT DISULFID 65 94
CC FT DISULFID 98 145
CC FT DISULFID 129 158
CC FT DISULFID 163 204
CC FT DISULFID 190 220
CC FT DISULFID 225 267
CC FT DISULFID 253 283
CC FT CARBOHYD 95 95
CC FT LIPID 353 353
CC FT VARSPIC 362 381
CC FT
CC FT VARIANT 52 52
CC FT
CC FT VARIANT 52 52
CC FT
CC FT VARIANT 82 82
CC FT
CC FT VARIANT 199 199
CC FT
CC FT VARIANT 227 227
CC FT
CC FT CONFLICT 80 80
CC FT CONFLICT 85 85
CC FT CONFLICT 187 187
CC FT CONFLICT 297 297
CC FT
CC SQ SEQUENCE 381 AA; 41388 MW; 29138EBB6B4B565E CRC64;
CC
CC Query Match 79.0%; Score 301; DB 1; Length 381;
CC Best Local Similarity 100.0%; Pred. NO. 1,4e-286; Indels 0; Gaps 0;
CC Matches 301; Conservative 0; Mismatches 0;
CC
CC QY 81 CLKGSQMSDIEFCNRSCEVPTRLNSASLSKOPYITQNTYPTGVYVEECRPGYRREPSLS 140
CC ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
CC DB 81 CLKGSQMSDIEFCNRSCEVPTRLNSASLSKOPYITQNTYPTGVYVEECRPGYRREPSLS 140

QY 141 PKLCLONLWKSTAVECKKSCNPGCIRNGQIDVPGILFGATISPSCTGKLGEST 200
 DB 141 PKLCLONLWKSTAVECKKSCNPGCIRNGQIDVPGILFGATISPSCTGKLGEST 200
 QY 201 SSFCLIGSSVQWSDPLPECEIYCPAPPOIDNGIGERDHYGROSVTACKNGFMI 260
 DB 201 SSFCLIGSSVQWSDPLPECEIYCPAPPOIDNGIGERDHYGROSVTACKNGFMI 260
 QY 261 GHSIYCTVNNDEGEWSPPECEKSKLSKVPPTVQKPTTVNPTTEVSPTSOKTTTKT 320
 DB 261 GHSIYCTVNNDEGEWSPPECEKSKLSKVPPTVQKPTTVNPTTEVSPTSOKTTTKT 320
 QY 321 TTPNAOATFRSTPVSRPTKHFHTTPNKGSGTSGTTRLLSGHCPPLTGLGLVTMGLL 380
 DB 321 TTPNAOATFRSTPVSRPTKHFHTTPNKGSGTSGTTRLLSGHCPPLTGLGLVTMGLL 380
 QY 381 T 381
 DB 381 T 381

RESULT 2
 DAF_PONPY STANDARD; PRT; 340 AA.
 AC P49457;
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Complement decay-accelerating factor (CD55) (Fragment).
 GN DAF OR CD55.
 OS Pongo pygmaeus (Orangutan).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Pongo.
 OX NCBI_TaxID=9600.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=94110622; PubMed=7506731;
 RA Nickells M.W., Alvarez J.I., Ludlin D.M., Atkinson J.P.;
 RT "Characterization of DAF-2, a high molecular weight form of decay-
 accelerating factor (DAF, CD55), as a covalently cross-linked dimer
 of DAF-1.";
 RL J. Immunol. 152:676-685(1994).
 CC -1- FUNCTION: THIS PROTEIN RECOGNIZES C4B AND C3B FRAGMENTS THAT
 CONDENSE WITH CELL-SURFACE HYDROXYL OR AMINO GROUPS WHEN NASCENT
 C4B AND C3B ARE LOCALLY GENERATED DURING C4 AND C3 ACTIVATION.
 CC INTERACTION OF DAF WITH CELL-ASSOCIATED C4B AND C3B POLYPEPTIDES
 CC INTERFERES WITH THEIR ABILITY TO CATALYZE THE CONVERSION OF C2 AND
 CC FACTOR B TO ENZYMATICALLY ACTIVE C2A AND Bb AND THEREBY PREVENTS
 CC THE FORMATION OF C4B2A AND C3BBb, THE AMPLIFICATION CONVERTASES OF
 CC THE COMPLEMENT CASCADE (BY SIMILARITY).
 CC -1- SUBUNIT: MONOMER (MAJOR FORM) AND NON-DISULFIDE-LINKED, COVALENT
 CC HOMODIMER (MINOR FORM).
 CC -1- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor.
 CC -1- ALTERNATIVE PRODUCTS: 2 isoforms; DAF-1 and DAF-2 (shown here);
 CC are produced by alternative splicing.
 CC -1- DOMAIN: THE FIRST SUSHI DOMAIN (SCR1) IS NOT NECESSARY FOR
 CC FUNCTION. SCR2 AND SCR4 PROVIDE THE PROPER CONFORMATION FOR THE
 CC ACTIVE SITE ON SCR3 (BY SIMILARITY).
 CC -1- PTM: THE SER/THR-RICH DOMAIN IS HEAVILY O-GLYCOSYLATED.
 CC -1- SIMILARITY: CONTAINS 4 SUSHI (SCR) DOMAINS.
 CC -1- SIMILARITY: BELONGS TO THE RECEPTORS OF COMPLEMENT ACTIVATION
 CC (RCA) FAMILY.
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 CC -----
 CC EMBL; S67775; AAC60609.1; -.
 CC HSSP; P08603; IHFI.

DR InterPro: IPR000436; Sushi_SCR_CCP.
 DR Pfam: PF00084; sushi; 4.
 DR SMART: SM00032; CCP; 4.
 KW Complement pathway; Plasma; Glycoprotein; Membrane; Repeat;
 KW Alternative splicing; GPI-anchor; Sushi.
 FT NON_TER 1 1
 FT CHAIN <1 312
 FT PROPEP 313 340
 FT DOMAIN <1 54
 FT DOMAIN 56 118
 FT DOMAIN 121 180
 FT DOMAIN 183 243
 FT DOMAIN 246 315
 FT DISULFID 24 53
 FT DISULFID 57 104
 FT DISULFID 88 117
 FT DISULFID 122 163
 FT DISULFID 149 179
 FT DISULFID 184 226
 FT DISULFID 212 242
 FT CARBOHYD 54 54
 FT CARBOHYD 107 107
 FT LIPID 312 312
 SQ SEQUENCE 340 AA; 37180 MW; D3D865C058204290 CRC64;
 Query Match 22.3%; Score 85; DB 1; Length 340;
 Best Local Similarity 100.0%; Pred. No. 2,5e-75;
 Matches 85; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 272 DEGEWSPPECEKSKLSKVPPTVQKPTTVNPTTEVSPTSOKTTTKTTPNAOATRST 331
 DB 231 DEGEWSPPECEKSKLSKVPPTVQKPTTVNPTTEVSPTSOKTTTKTTPNAOATRST 290
 QY 332 PVSRTKHFHTTPNKGSGTSGTT 356
 DB 291 PVSRTKHFHTTPNKGSGTSGTT 315

RESULT 3
 DAF_CAVPO STANDARD; PRT; 507 AA.
 AC Q60401; Q60402; Q60403; Q60404; Q60405; Q60406; P97254; P97255;
 AC P97256; Q9W719;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Complement decay-accelerating factor precursor.
 GN DAF.
 OS Cavia porcellus (Guinea pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Hystriognathi; Cavidae; Cavia.
 OX NCBI_TaxID=10141.
 RN [1]
 RP SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
 RC STRAIN=Hartley; Tissue=Spleen;
 RX MEDLINE=95403978; PubMed=7545710;
 RA Nonaka M., Miwa T., Okada N., Nonaka M., Okada H.;
 RT "Multiple isoforms of guinea pig decay-accelerating factor (DAF)
 RT generated by alternative splicing.";
 RL J. Immunol. 155:3037-3048(1995).
 CC -1- FUNCTION: PREVENTS THE FORMATION AND/OR ACCELERATES THE
 CC DISSOCIATION OF C3 CONVERTASE.
 CC -1- SUBCELLULAR LOCATION: ATTACHED TO THE MEMBRANE BY A GPI-ANCHOR
 CC (ISOFORM 3); SECRETED (ISOFORMS 4).
 CC -1- ALTERNATIVE PRODUCTS: At least 7 isoforms; 1 (shown here), 2/GDA-
 CC TCS, 3/GDAB-GPI, 4/GDAB-SEC, 5/GDAB-TCL, 6/GDAB-TCL and 7/GDAB-
 CC TCS; are produced by alternative splicing. GDAB-SEC is the
 CC secreted form, GDAB-TCL and GDAB-TCS have a longer cytoplasmic
 CC region, GDA-TCS and GDAB-TCS have a shorter cytoplasmic region and
 CC GDAB-GPI is the GPI-anchored form.
 CC -1- TISSUE SPECIFICITY: ALL THE ISOFORMS ARE WIDELY EXPRESSED. GPI AND
 CC TCS ARE THE MAJOR FORMS, WHEREAS SEC IS MINOR AND TCL IS ONLY
 CC PRESENT IN TRACE LEVELS.

CC	-1- SIMILARITY: CONTAINS 4 SUSPI (SCR) DOMAINS.
CC	-1- SIMILARITY: BELONGS TO THE RECEPTORS OF COMPLEMENT ACTIVATION
CC	(RCA) FAMILY.
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CC	-----
DR	EMBL; D55667; BAA09514.1; -
DR	EMBL; D55656; BAA09514.1; JOINED.
DR	EMBL; D55667; BAA09514.1; JOINED.
DR	EMBL; D55658; BAA09514.1; JOINED.
DR	EMBL; D55659; BAA09514.1; JOINED.
DR	EMBL; D55660; BAA09514.1; JOINED.
DR	EMBL; D55661; BAA09514.1; JOINED.
DR	EMBL; D55662; BAA09514.1; JOINED.
DR	EMBL; D55663; BAA09518.1; JOINED.
DR	EMBL; D55664; BAA09514.1; JOINED.
DR	EMBL; D55665; BAA09514.1; JOINED.
DR	EMBL; D55667; BAA09514.1; JOINED.
DR	EMBL; D55668; BAA09515.1; JOINED.
DR	EMBL; D55657; BAA09515.1; JOINED.
DR	EMBL; D55669; BAA09515.1; JOINED.
DR	EMBL; D55659; BAA09515.1; JOINED.
DR	EMBL; D55660; BAA09515.1; JOINED.
DR	EMBL; D55661; BAA09515.1; JOINED.
DR	EMBL; D55662; BAA09515.1; JOINED.
DR	EMBL; D55663; BAA09515.1; JOINED.
DR	EMBL; D55664; BAA09515.1; JOINED.
DR	EMBL; D55665; BAA09515.1; JOINED.
DR	EMBL; D55667; BAA09515.1; JOINED.
DR	EMBL; D55656; BAA09516.1; JOINED.
DR	EMBL; D55657; BAA09516.1; JOINED.
DR	EMBL; D55658; BAA09516.1; JOINED.
DR	EMBL; D55659; BAA09516.1; JOINED.
DR	EMBL; D55660; BAA09516.1; JOINED.
DR	EMBL; D55661; BAA09517.1; JOINED.
DR	EMBL; D55662; BAA09517.1; JOINED.
DR	EMBL; D55663; BAA09517.1; JOINED.
DR	EMBL; D55664; BAA09517.1; JOINED.
DR	EMBL; D55665; BAA09517.1; JOINED.
DR	EMBL; D55666; BAA09517.1; JOINED.
DR	EMBL; D55667; BAA09518.1; JOINED.
DR	EMBL; D55656; BAA09518.1; JOINED.
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DR <th>EMBL</th> <th>D55661</th> <th>BAA09519.1</th> <th>JOINED</th>	EMBL	D55661	BAA09519.1	JOINED
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OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 ON NCBI_TaxId=10090;
 RX [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Testis;
 RX MEDLINE=95403982; Pubmed=7545711;
 RA Spicer A.P., Seldin M.F., Gendler S.J.;
 RT "Molecular cloning and chromosomal localization of the mouse decay-
 RT accelerating factor genes. Duplicated genes encode
 RT glycosylphosphatidylinositol-anchored and transmembrane forms.";
 RL J. Immunol. 153:3079-3091(1995).
 RN [12]
 RP SEQUENCE OF 7-390 FROM N.A.
 RC STRAIN=BALB/c; TISSUE=Spleen;
 RX MEDLINE=96362213; Pubmed=8671624;
 RA Fukuda Y., Yasui A., Okada N., Okada H.;
 RT "Immunoscreening of murine decay accelerating factor by
 RT Int. Immunol. 8:379-385(1996).
 CC -1- FUNCTION: PROTECTION OF CELLS FROM COMPLEMENT-MEDIATED DAMAGE (BY
 CC SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor.
 CC -1- TISSUE SPECIFICITY: BRAIN, SECRETORY EPITHELIA, SKELETAL MUSCLE,
 CC LIVER, TESTES, THYMUS, SPLEEN AND LYMPH NODE.
 CC -1- DOMAIN: THE FIRST SUSHI DOMAIN (SCR1) IS NOT NECESSARY FOR
 CC FUNCTION. SCR2 AND SCR4 PROVIDE THE PROPER CONFORMATION FOR THE
 CC ACTIVE SITE ON SCR3 (BY SIMILARITY).
 CC -1- SIMILARITY: CONTAINS 4 SUSHI (SCR) DOMAINS.
 CC -1- SIMILARITY: BELONGS TO THE RECEPTORS OF COMPLEMENT ACTIVATION
 CC (RCA) FAMILY.
 CC -----
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 CC -----
 DR EMBL: LA1366; AAB00092.1; -;
 DR EMBL: D63679; BAA09830.1; -;
 DR HSSP: P08603; IHCC.
 DR MGD: MGI:104850; Daf1.
 DR InterPro: IPR000436; Sushi_SCR_CCP.
 DR Pfam: PF00084; sushi; 4.
 DR SMART: SM00032; CCP; 4.
 KW Complement pathway; Glycoprotein; Membrane; Repeat; GPI-anchor;
 KW Signal; Sushi.
 FT SIGNAL 1 34
 FT CHAIN 35 361
 FT PROPER 362 390
 FT DOMAIN 35 95
 FT DOMAIN 97 159
 FT DOMAIN 162 221
 FT DOMAIN 224 285
 FT DOMAIN 288 364
 FT DISULFID 65 94
 FT DISULFID 98 145
 FT DISULFID 129 158
 FT DISULFID 163 204
 FT DISULFID 190 220
 FT DISULFID 225 267
 FT DISULFID 253 284
 FT CARBOHYD 187 187
 FT CARBOHYD 262 262
 FT LIPID 361 361
 FT CONFLICT 9 7
 FT CONFLICT 83 9
 FT CONFLICT 91 91
 E -> G (IN REF. 2).
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 E -> G (IN REF. 2).

FT CONFLICT 135 135 E -> K (IN REF. 2).
 FT CONFLICT 173 173 H -> L (IN REF. 2).
 FT CONFLICT 180 180 I -> T (IN REF. 2).
 SQ SEQUENCE 390 AA; 42618 MW; 4418721DFF47F8E7 CRC64;
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 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 157 FCKRKSQPNP 166
 DB 157 FCKRKSQPNP 166
 RESULT 5
 DAF2_MOUSE
 ID DAF2_MOUSE STANDARD; PRT; 407 AA.
 AC 061476;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE Complement decay-accelerating factor, transmembrane precursor
 DE (DAF-TM).
 GN DAF2.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 ON NCBI_TaxId=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Testis;
 RX MEDLINE=95403982; Pubmed=7545711;
 RA Spicer A.P., Seldin M.F., Gendler S.J.;
 RT "Molecular cloning and chromosomal localization of the mouse decay-
 RT accelerating factor genes. Duplicated genes encode
 RT glycosylphosphatidylinositol-anchored and transmembrane forms.";
 RL J. Immunol. 153:3079-3091(1995).
 CC -1- FUNCTION: PROTECTION OF CELLS FROM COMPLEMENT-MEDIATED DAMAGE (BY
 CC SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein (Potential).
 CC -1- TISSUE SPECIFICITY: TESTIS, SPLEEN AND LYMPH NODE.
 CC -1- DOMAIN: THE FIRST SUSHI DOMAIN (SCR1) IS NOT NECESSARY FOR
 CC FUNCTION. SCR2 AND SCR4 PROVIDE THE PROPER CONFORMATION FOR THE
 CC ACTIVE SITE ON SCR3 (BY SIMILARITY).
 CC -1- SIMILARITY: CONTAINS 4 SUSHI (SCR) DOMAINS.
 CC -1- SIMILARITY: BELONGS TO THE RECEPTORS OF COMPLEMENT ACTIVATION
 CC (RCA) FAMILY.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: LA1365; AAB00092.1; -;
 DR HSSP: P08603; IHCC.
 DR MGD: MGI:104849; Daf2.
 DR InterPro: IPR000436; Sushi_SCR_CCP.
 DR Pfam: PF00084; sushi; 4.
 DR SMART: SM00032; CCP; 4.
 KW Complement pathway; Glycoprotein; Repeat; Signal; Sushi;
 KW Transmembrane.
 FT SIGNAL 1 39
 FT CHAIN 40 407
 FT DOMAIN 40 368
 FT TRANSMEM 369 389
 FT DOMAIN 390 407
 FT DOMAIN 40 100
 FT DOMAIN 102 164
 FT DOMAIN 167 226
 SUSHI 1.
 SUSHI 2.
 SUSHI 3.

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FT DOMAIN 229 290 SUSHI 4.
FT DOMAIN 291 363 SER/THR-RICH (BY SIMILARITY).
FT DISULFID 70 99 BY SIMILARITY.
FT DISULFID 103 150 BY SIMILARITY.
FT DISULFID 134 163 BY SIMILARITY.
FT DISULFID 168 209 BY SIMILARITY.
FT DISULFID 195 225 BY SIMILARITY.
FT DISULFID 230 272 BY SIMILARITY.
FT DISULFID 258 289 BY SIMILARITY.
FT CARBOHYD 192 192 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 267 267 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 407 AA; 44469 MW; DDD82FD72CEAD40 CRC64;

Query Match 2.6%; Score 10; DB 1; Length 407;
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Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 157 FCKKSCPNP 166
DB 162 FCKKSCPNP 171

RESULT 6
APOH_HUMAN STANDARD: PRT: 345 AA.
ID APOH_HUMAN P02749:
AC 21-JUL-1986 (Rel. 01, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Beta-2-glycoprotein I precursor (Apolipoprotein H) (Apo-H) (B2GPI)
DE (Beta(2)GPI) (Activated protein C-binding protein) (APC inhibitor).
GN APOH OR B2GI.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
[1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE-91315408; PubMed-1650181;
RA Steinkasserer A., Estaller C., Weiss E., Sim R.B., Day A.J.;
RT "Complete nucleotide and deduced amino acid sequence of human beta 2-
RT glycoprotein I.";
RL Biochem. J. 277:387-391(1991).
[2]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE-92008618; PubMed-1655523;
RA Kristensen T., Schousboe I., Boel E., Mulvihill E.M., Hansen R.R.,
RA Moeller K.B., Moeller N.P.H., Sottrup-Jensen L.;
RT "Molecular cloning and mammalian expression of human beta
RT 2-glycoprotein I cDNA.";
RL FEBS Lett. 289:183-186(1991).
[3]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE-92084151; PubMed-1748314;
RA Mehdi H., Nunn M., Steel D.M., Whitehead A.S., Perez M., Walker L.,
RA Peebles M.E.;
RT "Nucleotide sequence and expression of the human gene encoding
RT apolipoprotein H (beta 2-glycoprotein I).";
RL Gene 108:293-298(1991).
[4]
RP SEQUENCE FROM N.A.
RX MEDLINE-92273779; PubMed-1339416;
RA Day J.R., O'Hara P.J., Grant F.J., Lofton-Day C.E., Berkaw M.N.,
RA Werner P., Arnard P.;
RT "Molecular cloning and sequence analysis of the cDNA encoding human
RT apolipoprotein H (beta 2-glycoprotein I).";
RL Int. J. Clin. Lab. Res. 21:256-263(1992).
[5]
RP SEQUENCE FROM N.A.
RX MEDLINE-92135065; PubMed-177418;
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RA Matsura E., Igarashi M., Igarashi Y., Nagae H., Ichikawa K.,
RA Yasuda T., Koike T.;
RT "Molecular definition of human beta 2-glycoprotein I (beta 2-GPI) by
RT cDNA cloning and inter-species differences of beta 2-GPI in
RT alternation of anticardiolipin binding.";
RL Int. Immunol. 3:1217-1221(1991).
[6]
RP SEQUENCE FROM N.A.
RX MEDLINE-99115472; PubMed-9914524;
RA Okkels H., Rasmussen T.E., Sanghera D.K., Kamboh M.I., Kristensen T.;
RT "Structure of the human beta2-glycoprotein I (apolipoprotein H)
RT gene.";
RL Eur. J. Biochem. 259:435-440(1999).
[7]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RA Strausberg R.;
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
[8]
RP SEQUENCE OF 20-345, CARBOHYDRATE-LINKAGE SITES, AND DISULFIDE BONDS.
RX MEDLINE-84222015; PubMed-6587378;
RA Lozler J., Takahashi N., Putnam F.W.;
RT "Complete amino acid sequence of human plasma beta 2-glycoprotein I.";
RL Proc. Natl. Acad. Sci. U.S.A. 81:3640-3644(1984).
[9]
RP SEQUENCE OF 20-38.
RC TISSUE-Follicular fluid;
RX MEDLINE-21148139; PubMed-11250549;
RA Aleporou-Marinou V., Pappa H., Yalouris P., Patargias T.;
RT "Purification of apolipoprotein H (beta 2-glycoprotein I)-like protein
RT from human follicular fluid.";
RL Comp. Biochem. Physiol. 128B:537-542(2001).
[10]
RP DISULFIDE BONDS IN C-TERMINAL DOMAIN.
RX MEDLINE-93050249; PubMed-1426288;
RA Steinkasserer A., Barlow P.N., Willis A.C., Kertesz Z.,
RA Campbell I.D., Sim R.B., Norman D.G.;
RT "Activity, disulphide mapping and structural modelling of the fifth
RT domain of human beta 2-glycoprotein I.";
RL FEBS Lett. 313:193-197(1992).
[11]
RP STRUCTURE OF CARBOHYDRATES.
RX MEDLINE-97299942; PubMed-915091;
RA Gambino R., Rulu G., Pagano G., Cassader M.;
RT "Qualitative analysis of the carbohydrate composition of
RT apolipoprotein H.";
RL J. Protein Chem. 16:205-212(1997).
[12]
RP X-RAY CRYSTALLOGRAPHY (2.7 ANGSTROMS).
RC TISSUE=Plasma;
RX MEDLINE-99437994; PubMed-10508150;
RA Bouna B., de Groot P.G., van Den Elsen J.M.H., Ravelli R.B.G.,
RA Schouten A., Simmelink M.J.A., Derksen R.H.W.M., Kroon J., Gros P.;
RT "Adhesion mechanism of human beta(2)-glycoprotein I to phospholipids
RT based on its crystal structure.";
RL EMBO J. 18:5166-5174(1999).
[13]
RP X-RAY CRYSTALLOGRAPHY (2.87 ANGSTROMS).
RX MEDLINE-20031634; PubMed-10562535;
RA Schwarzenbacher R., Zeth K., Diederichs K., Gries A., Kostner G.M.,
RA Laggner P., Prassl R.;
RT "Crystal structure of human beta2-glycoprotein I: implications for
RT phospholipid binding and the antiphospholipid syndrome.";
RL EMBO J. 18:6228-6239(1999).
[14]
RP VARIANT LEU-266.
RX MEDLINE-93273313; PubMed-8099061;
RA Steinkasserer A., Doerner C., Wuerzner R., Sim R.B.;
RT "Human beta 2-glycoprotein I: molecular analysis of DNA and amino
RT acid polymorphism.";
RL Hum. Genet. 91:401-402(1993).
[15]
RP VARIANT ASN-107.
```

RX MEDLINE-97369481; PubMed-9225969;
 RA Sanghera D.K., Kristensen T., Hamman R.F., Kamboh M.I.;
 RT "Molecular basis of the apolipoprotein H (beta 2-glycoprotein I)
 RT protein polymorphism";
 RL Hum. Genet. 100:57-62(1997).
 RN [16]
 RP VARIANTS GLY-325 AND SER-335;
 RX MEDLINE-97217791; PubMed-9063752;
 RA Sanghera D.K., Magenhecht D.R., McInyre J.A., Kamboh M.I.;
 RT "Identification of structural mutations in the fifth domain of
 RT apolipoprotein H (beta 2-glycoprotein I) which affect phospholipid
 RT binding";
 RL Hum. Mol. Genet. 6:311-316(1997).
 CC -1- FUNCTION: BINDS TO VARIOUS KINDS OF NEGATIVELY CHARGED SUBSTANCES
 CC SUCH AS HEPARIN, PHOSPHOLIPIDS, AND DEXTRAN SULFATE. MAY PREVENT
 CC ACTIVATION OF THE INTRINSIC BLOOD COAGULATION CASCADE BY BINDING
 CC TO PHOSPHOLIPIDS ON THE SURFACE OF DAMAGED CELLS.
 CC -1- TISSUE SPECIFICITY: PLASMA.
 CC -1- SIMILARITY: CONTAINS 4 SUSHI (SCR) DOMAINS.
 CC -----
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 CC -----
 CC
 DR EMBL: X58100; CAA41113.1; -;
 DR EMBL: X53595; CAA37664.1; -;
 DR EMBL: X57847; CAA40977.1; -;
 DR EMBL: M62839; AAA51766.1; -;
 DR EMBL: S80305; AAB21330.1; -;
 DR EMBL: Y11493; CAA72279.1; -;
 DR EMBL: Y11494; CAA72279.1; JOINED.
 DR EMBL: Y11495; CAA72279.1; JOINED.
 DR EMBL: X53595; CAA72279.1; JOINED.
 DR EMBL: Y11496; CAA72279.1; JOINED.
 DR EMBL: Y11497; CAA72279.1; JOINED.
 DR EMBL: Y11498; CAA72279.1; JOINED.
 DR EMBL: Y17754; CAA76845.1; -;
 DR EMBL: BC020703; AAH20703.1; -;
 DR PIR: S17178; B43286.
 DR PIR: B43286; B43286.
 DR PDB: LOUB: 08-OCT-99.
 DR PDB: 1C12; 19-NOV-99.
 DR Genew; HGNC:616; APOH.
 DR MIM; 138700; -;
 DR InterPro: IPR000436; Sush1_SCR.CCP.
 DR Pfam: PF00084; sush1; 4.
 DR SMART: SM00032; CCP; 4.
 KW Heparin-binding; Glycoprotein; Plasma; Repeat; Sush1; Signal;
 KW Polymorphism; 3D-structure.
 FT STGNL 1 19
 FT CHAIN 20 345 BETA-2-GLYCOPROTEIN I.
 FT DOMAIN 22 80 SUSHI 1.
 FT DOMAIN 83 138 SUSHI 2.
 FT DOMAIN 141 201 SUSHI 3.
 FT DOMAIN 204 261 SUSHI 4.
 FT DOMAIN 263 345 SUSHI-LIKE.
 FT DISULFID 23 66
 FT DISULFID 51 79
 FT DISULFID 84 124
 FT DISULFID 110 137
 FT DISULFID 142 188
 FT DISULFID 174 200
 FT DISULFID 205 248
 FT DISULFID 234 260
 FT DISULFID 264 315
 FT DISULFID 300 325
 FT DISULFID 307 345
 FT CARBOHYD 149 149
 FT CARBOHYD 162 162
 O-LINKED.
 N-LINKED (GLCNAC. .).

FT CARBOHYD 183 183 N-LINKED (GLCNAC. .).
 FT CARBOHYD 193 193 N-LINKED (GLCNAC. .).
 FT CARBOHYD 253 253 N-LINKED (GLCNAC. .).
 FT VARIANT 107 107 S-> N (IN APOH*1).
 FT /FTID=VAR_008169.
 Query Match 2.4%; Score 9; DB 1; Length 345;
 Best Local Similarity 100.0%; Pred. No. 0.56;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 185 TISFSCNTG 193
 Db 105 TISFSCNTG 113
 RESULT 7
 ID TAL_PSEAE STANDARD; PRT; 307 AA.
 AC 091047;
 DT 15-JUN-2002 (Rel. 41, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DE 15-JUN-2002 (Rel. 41, Last annotation update)
 GN TAL OR PA2796.
 OS Pseudomonas aeruginosa.
 OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
 OC Pseudomonas
 NCBI_TaxID=287;
 OX
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 15692 / PA01;
 RX MEDLINE-20437337; PubMed-10984043;
 RA Stover C.K., Pham X.-O.T., Erwin A.L., Mizoguchi S.D., Warren P.,
 RA Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,
 RA Garner R.L., Goltzy L., Tolerino E., Westbrock-Wadman S., Yuan Y.,
 RA Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,
 RA Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
 RA Reizer J., Sailer M.H., Hancock R.E.W., Lory S., Olson M.V.;
 RA "Complete genome sequence of Pseudomonas aeruginosa PA01, an
 RT opportunistic pathogen";
 RT Nature 406:959-964(2000).
 RL Nature 406:959-964(2000).
 CC -1- FUNCTION: Transaldolase is important for the balance of
 CC metabolites in the pentose-phosphate pathway (by similarity).
 CC -1- CATALYTIC ACTIVITY: Sedoheptulose 7-phosphate + D-glyceraldehyde
 CC 3-phosphate -> D-erythrose 4-phosphate + D-fructose 6-phosphate.
 CC -1- PATHWAY: Pentose phosphate pathway; nonoxidative part.
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic (Probable).
 CC -1- SIMILARITY: BELONGS TO THE TRANSALDOLASE FAMILY, SUBFAMILY 1.
 CC -----
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 CC -----
 CC
 DR EMBL: AE004707; AAC06184.1; -;
 DR HSSP: P30148; IONR.
 DR InterPro: IPR001585; Transaldolase.
 DR InterPro: IPR004730; Transaldolase_AB.
 DR Pfam: PF00923; Transaldolase; 1.
 DR TIGRPFAM: TIGR00874; talAB; 1.
 DR PROSITE: PS01054; TRANSALDOLASE_1; 1.
 DR PROSITE: PS00958; TRANSALDOLASE_2; 1.
 KW Transferrase; Pentose shunt; Complete proteome.
 FT ACT_SITE 125 125 BY SIMILARITY.
 SO SEQUENCE 307 AA; 33946 MW; 840B2B6AF288594 CRC64;
 Query Match 2.1%; Score 8; DB 1; Length 307;
 Best Local Similarity 100.0%; Pred. No. 4.8;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DR EMBL: AF035664; AAD02042.1; JOINED.
 DR EMBL: AF035665; AAD02042.1; JOINED.
 DR EMBL: AF035666; AAD02042.1; JOINED.
 DR EMBL: AF035667; AAD02042.1; JOINED.
 DR EMBL: AF035668; AAD02042.1; JOINED.
 DR EMBL: AF035669; AAD02042.1; JOINED.
 DR PDB: 1TBI; 08-NOV-96.
 DR Genew; HGNC:11772; TGFBR1.
 DR MIM; 190181; -.
 DR InterPro: IPR000472; Activin_rec.
 DR InterPro: IPR000719; Euk_pkinase.
 DR InterPro: IPR002280; Ser_thr_pkinase.
 DR Pfam: PF00069; pkinase; 1.
 DR Pfam: PF01064; Activin_rec; 1.
 DR Prodom: PD000001; Euk_pkinase; 1.
 DR SMART: SM00467; GS; 1.
 DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
 DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
 DR Receptor; Transferase; Serine/threonine-protein kinase; ATP-binding;
 KM Transmembrane; Glycoprotein; Signal; 3D-structure.
 FT SIGNAL 1 24
 FT CHAIN 25 503
 FT DOMAIN 25 125
 FT TRANSMEM 126 147
 FT DOMAIN 148 503
 FT DOMAIN 205 495
 FT NE_BIND 211 219
 FT BINDING 232 232
 FT ACT_SITE 333 333
 FT CARBOHYD 45 45
 FT DISULFID 36 54
 FT DISULFID 38 41
 FT DISULFID 48 71
 FT DISULFID 86 100
 FT DISULFID 101 106
 SQ SEQUENCE 503 AA; 55959 MW; 179F11404725DDCB CRC64;

Query Match 2.1%; Score 8; DB 1; Length 503;
 Best Local Similarity 100.0%; Pred. No. 7.3;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 19 PRLLLV 26
 Db 10 PRLLLV 17
 RESULT 10
 PME_PRUPE
 ID PME_PRUPE STANDARD; PRT; 522 AA.
 AC 043062;
 DT 15-JUL-1999 (Rel. 38, Created)
 DT 15-JUL-1999 (Rel. 38, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Pectinesterase P88B precursor (EC 3.1.1.11) (Pectin methylsterase)
 DE (PE).
 OS Prunus persica (Peach).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
 OC eucosids I; Rosales; Rosaceae; Amygdaloideae; Prunus.
 OX NCBI_TaxID=3760;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Coronet; TISSUE=Fruit;
 RA Glover H., Brady C.J., Lee E., Speirs J.;
 RT "Multiple pectin esterase genes are expressed in ripening peach fruit:
 RT nucleotide sequence of a cDNA encoding peach pectin esterase.";
 RL (In) Plant Gene Register PG896-094
 CC "- FUNCTION: MAY HAVE ROLES IN THE DEPOSITION OF PECTIN IN DEVELOPING
 CC TISSUES AND IN THE WALL LOOSENING AND CELL SEPARATION THAT OCCURS
 CC IN CELL EXPANSION, FRUIT RIPENING AND ABSCISSION."
 CC "- CATALYTIC ACTIVITY: Pectin + N H(2)O = N methanol + pectate.

CC -1- DEVELOPMENTAL STAGE: PRESENT THROUGHOUT FRUIT DEVELOPMENT.
 CC -1- SIMILARITY: BELONGS TO THE PECTINESTERASE FAMILY.
 CC -1- CAUTION: IT IS UNCERTAIN WHETHER MET-1, MET-6 IS THE INITIATOR.
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 CC
 DR EMBL: X95991; CAA65237.1; -.
 DR InterPro: IPR000070; Pectinesterase.
 DR Pfam: PF01095; Pectinesterase; 1.
 DR PROSITE: PS00800; PECTINESTERASE_1; 1.
 DR PROSITE: PS00503; PECTINESTERASE_2; 1.
 DR Signal; Hydrolase; Aspartyl esterase; Cell wall; Glycoprotein;
 KW Multigene family.
 FT SIGNAL 1 30
 FT CHAIN 31 522
 FT DOMAIN 253 256
 FT ACT_SITE 336 336
 FT ACT_SITE 357 357
 FT CARBOHYD 105 105
 FT CARBOHYD 118 118
 FT CARBOHYD 119 119
 FT CARBOHYD 218 218
 FT CARBOHYD 221 221
 FT CARBOHYD 224 224
 FT CARBOHYD 405 405
 FT CARBOHYD 489 489
 FT CARBOHYD 496 496
 SQ SEQUENCE 522 AA; 57396 MW; 6F9211A516C7949A CRC64;

Query Match 2.1%; Score 8; DB 1; Length 522;
 Best Local Similarity 100.0%; Pred. No. 7.5;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 21 LLLLVLC 28
 Db 18 LLLLVLC 25
 RESULT 11
 UL25_HSV62
 ID UL25_HSV62 STANDARD; PRT; 555 AA.
 AC P52537;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Virion protein U50.
 DE Virion protein U50.
 GN U50 OR KAI1R.
 OS Human herpesvirus (type 6 / strain 229) (HHV6).
 OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
 OC Betaherpesvirinae; Roseoloviruses.
 OX NCBI_TaxID=36351;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=95074921; Pubmed=7983761;
 RA Stamey F.R., Dominguez G., Black J.B., Dambaugh T.R., Pellett P.E.;
 RT "Intragenomic linear amplification of human herpesvirus 6B orlyt
 RT suggests acquisition of orlyt by transposition.";
 RL J. Virol. 69:589-596(1995).
 CC "- FUNCTION: VIRION PROTEIN.
 CC -1- SIMILARITY: BELONGS TO FAMILY THAT GROUPS TOGETHER HSV-1 UL25,
 CC EBV-1 36, EBV BVRF1, HCMV UL77, ILTV ORF2, AND VZV 34.
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CC -----

DR EMBL: AF157706; AAB06348.1; -

DR InterPro: IPR002493; UL25.

DR Pfam: PF01499; UL25; 1.

DR SEQUENCE 555 AA; 63830 MW; 68B86590DC4CD2BC CRC64;

Query Match 2.1%; Score 8; DB 1; Length 555;
Best Local Similarity 100.0%; Pred. No. 7.9;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 71 KIPGEKDS 78
Db 311 KIPGEKDS 318

RESULT 12

CABP_RAT
ID CABP_RAT STANDARD; PRT; 558 AA.

AC 063514;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE CAB-binding protein alpha chain precursor (c4bp).
GN C4BPA.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
RN NCBI_TaxID=10116;
[1]

RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley; TISSUE=Liver;
RX MEDLINE=9716082; PubMed=9013975;
RA Hillarp A., Wiklund H., Thern A., Dahlback B.;
RT "Molecular cloning of rat C4b binding protein alpha- and beta-chains:
structural and functional relationships among human, bovine, rabbit,
mouse, and rat proteins.";
RL J. Immunol. 158:1315-1323(1997).

CC -1- FUNCTION: C4BP CONTROLS THE CLASSICAL PATHWAY OF COMPLEMENT
ACTIVATION. IT BINDS AS A COFACTOR TO C3B/C4B INACTIVATOR
(C3BINA), WHICH THEN HYDROLYZES THE COMPLEMENT FRAGMENT C4B. IT
CC ALSO ACCELERATES THE DEGRADATION OF THE C4B2A COMPLEX (C3
CC CONVERTASE) BY DISSOCIATING THE COMPLEMENT FRAGMENT C2A. ALPHA
CC CHAIN BINDS C4B. IT INTERACTS ALSO WITH ANTICOAGULANT PROTEIN S
CC AND WITH SERUM AMYLOID P COMPONENT.
CC -1- SUBUNIT: DISULFIDE-LINKED COMPLEX OF C4BP ALPHA AND BETA CHAINS.
CC -1- SIMILARITY: TO C4BP BETA CHAIN AND TO PTG APOLIPOPROTEIN R.
CC -1- SIMILARITY: CONTRAINS 8 SUSHI (SCR) DOMAINS.

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CC -----

DR EMBL: Z50051; CAA90391.1; -

DR HSSP: P10998; 1VD.

DR InterPro: IPR000436; Sushi_SCR_CCP.

DR Pfam: PF00084; sushi; 8.

DR SMART: SM00032; CCP; 8.

KN Complement pathway; Plasma; Glycoprotein; Repeat; Sushi; Signal.

FT SIGNAL 1 13
FT CHAIN 14 558 CAB-BINDING PROTEIN ALPHA CHAIN.
FT DOMAIN 14 73 SUSHI 1.
FT DOMAIN 76 73 SUSHI 2.
FT DOMAIN 138 135 SUSHI 3.
FT DOMAIN 203 200 SUSHI 4.
FT DOMAIN 262 325 SUSHI 5.
FT DOMAIN 328 387 SUSHI 6.
FT DOMAIN 389 444 SUSHI 7.

FT DOMAIN 446 502 SUSHI 8.
FT DISULFID 15 60 BY SIMILARITY.
FT DISULFID 45 72 BY SIMILARITY.
FT DISULFID 77 118 BY SIMILARITY.
FT DISULFID 104 134 BY SIMILARITY.
FT DISULFID 139 182 BY SIMILARITY.
FT DISULFID 168 199 BY SIMILARITY.
FT DISULFID 204 246 BY SIMILARITY.
FT DISULFID 232 258 BY SIMILARITY.
FT DISULFID 263 312 BY SIMILARITY.
FT DISULFID 296 324 BY SIMILARITY.
FT DISULFID 328 351 BY SIMILARITY.
FT DISULFID 329 373 BY SIMILARITY.
FT DISULFID 363 386 BY SIMILARITY.
FT DISULFID 390 431 BY SIMILARITY.
FT DISULFID 417 443 BY SIMILARITY.
FT DISULFID 447 488 BY SIMILARITY.
FT DISULFID 474 501 BY SIMILARITY.
FT DISULFID 509 509 INTERCHAIN (WITH BETA CHAIN) (POTENTIAL).
FT DISULFID 521 521 INTERCHAIN (WITH BETA CHAIN) (POTENTIAL).
FT CARBOHYD 31 31 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 177 177 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 186 186 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 469 469 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 491 491 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 558 AA; 62266 MW; 592F0C667ED15FF CRC64;

Query Match 2.1%; Score 8; DB 1; Length 558;
Best Local Similarity 100.0%; Pred. No. 8;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 213 WSDPLEC 220
Db 127 WSDPLEC 134

RESULT 13

RS15_PSEPU
ID RS15_PSEPU STANDARD; PRT; 89 AA.
AC 087791;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE 30S ribosomal protein S15.
GN RPSO.
OS Pseudomonas putida.
OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
OC Pseudomonas.
OX NCBI_TaxID=303;
[1]

RP SEQUENCE FROM N.A.
RC STRAIN=TMB;
RA Favaro R., Deno' G.;
RT "Identification and cloning of genes involved in RNA turnover in
RT Pseudomonas putida.";
RL Submitted (SEP-1998) to the EMBL/Genbank/DBJ databases.
CC -1- FUNCTION: THIS PROTEIN IS ONE OF THE 16S RIBOSOMAL RNA BINDING
CC PROTEINS (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE S15P FAMILY OF RIBOSOMAL PROTEINS.

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CC -----

DR EMBL: Y18132; CAA77047.1; -

DR HSSP: P80378; 1AB3.

DR InterPro: IPR005290; RS15_bact.

DR InterPro: IPR00589; Ribosomal_S15.

DR Pfam: PF00312; Ribosomal_S15; 1.

DR	TIGRFAMS; TIGR00952; S15_bact; 1.	FALSE_NEG.
KR	PROSITE; PS00362; RIBOSOMAL_S15.	FALSE_NEG.
DM	Ribosomal protein; rRNA-binding.	FALSE_NEG.
SO	SEQUENCE 89 AA; 9901 MW; 7CD73B1FE194EC4F	CRC64

Query Match	1.8%	Score 7:	DB 1:	length 89;
Best Local Similarity	100.0%	Pred. No. 16;		
Matches 7: Conservative	0;	Mismatches	0;	Indels 0;
QY 317 TTKTTP 323				
DB 46 TTKTTP 52				

```

RESULT 14
B2MG_CEBAL
ID      B2MG_CEBAL      STANDARD:      PRT:      119 AA.
AC      077826;
DT      30-MAY-2000 (Rel. 39, Created)
DT      30-MAY-2000 (Rel. 39, Last sequence update)
DT      30-MAY-2000 (Rel. 39, Last annotation update)
DE      Beta-2-microglobulin precursor.
GN      B2M.
OS      Cedus albifrons (White-fronted capuchin),
OS      Cedus apella (Brown-capped capuchin), and
OS      Cedus olivaceus (Weeper capuchin).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Cebinae; Cedus.
OX      NCBI_TaxID=9514, 9515, 37295;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      TISSUE=Blood;
RX      MEDLINE=98298008; PubMed=9634477;
RA      Canavez F.C., Ladasky J.J., Muniz J.A.P.C., Seunarez H.N., Parman P.;
RT      "Beta-2-microglobulin in neotropical primates (Platyrrhini).";
RL      Immunogenetics 48:133-140(1998).
CC      -1- FUNCTION: BETA-2-MICROGLOBULIN IS THE BETA-CHAIN OF MAJOR
CC      HISTOCOMPATIBILITY COMPLEX CLASS I MOLECULES.
CC      -1- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE DOMAIN.
CC      -----
CC      This SWISS-PROT entry is copyright. It is produced through a collaboration
CC      between the Swiss Institute of Bioinformatics and the EMBL outstation -
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```

Query Match	1.8%	Score 7;	DB 1;	Length 119;
Best Local	Similarity 100.0%;	Pred. No. 21;		
Matches 7;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

QY	23	LVVLVCL	29
Db	9	LVVLVCL	15

RESULT	15
B2MG_CHISA	
ID	B2MG_CHISA
STANDARD:	PRT: 119 AA.
AC	077532;
DT	15-DEC-1998 (Rel. 37, Created)
DT	15-DEC-1998 (Rel. 37, Last sequence update)
DT	15-JUN-2002 (Rel. 41, Last annotation update)
DE	Beta-2-microglobulin precursor.
GN	B2M.
OS	Chiropteres satanas (Black-bearded saki).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Pitheciinae;
OC	Chiropteres.
OX	NCBI_TaxID=9525;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	TISSUE=Blood;
FX	MEDLINE=98298008; PubMed=9634477;
RA	Canavez F.C., Ladasy J.J., Muniz J.A.P.C., Seunanez H.N., Parham P.;
RT	"Beta-2-microglobulin in neotropical primates (Platyrrhini).";
RL	Immunogenetics 48:133-140(1998).
CC	-1 FUNCTION: BETA-2-MICROGLOBULIN IS THE BETA-CHAIN OF MAJOR
CC	HISTOCOMPATIBILITY COMPLEX CLASS I MOLECULES.
CC	-1 SUBCELLULAR LOCATION: Secreted.
CC	-1 SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE DOMAIN.
CC	-----
CC	THIS SWISS-PROT entry is copyright. It is produced through a collaboration
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CC	entities requires a license agreement (see http://www.isb-sdb.ch/announce
CC	or send an email to license@isb-sdb.ch).
CC	-----
DR	EMBL; AF032075; AAC52097.1; -
DR	EMBL; AF032074; AAC52097.1; JOINED.
DR	HSSP; P01884; IAEZ.
DR	InterPro: IPR003006; IG_MHC.
DR	InterPro: IPR003597; IG-cl.
DR	Pfam; PF00047; Ig; 1.
DR	SMART; SM00407; Igc1; 1.
DR	PROSITE; PS00290; IG_MHC; FALSE_NEG.
KW	MHC 1; Signal.
FT	SIGNAL 1 20 BY SIMILARITY.
FT	CHAIN 21 119 BETA-2-MICROGLOBULIN.
FT	DISULFID 45 100 BY SIMILARITY.
SQ	SEQUENCE 119 AA; 13657 MW; BCCB591EFD6F3E CRC64;

Query Match	1.8%	Score 7	DB 1	Length 119
Best Local Similarity	100.0%	Pred. No. 21		
Matches	7	Conservative	0	Mismatches 0
				Indels 0
				Gaps 0
QY	23	LIVLCL	29	
DB	9	LIVLCL	15	

Search completed: February 12, 2003, 11:10:47
Job time : 16 secs

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GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: February 12, 2003, 11:08:01 ; Search time 38 Seconds
(without alignments)
1336.013 Million cell updates/sec

Title: US-09-623-035-2

Perfect score: 381

Sequence: 1 MVARPSVPAALPLGLGLPR.....HTCFLLTGLGLTWGLLT 381

Scoring table: OLIGO #
Gapop 60.0 , Gapext 60.0

Searched: 908470 seqs, 133250620 residues

Word size: 0

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database:

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23: /SIDS2/gcgdata/geneseq/genesqp-emb1/AA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	381	100.0	381	8 AAP70048	Human decay accele
2	381	100.0	381	16 AAP74773	Decay accelerating
3	381	100.0	381	16 AAR66683	Decay accelerating
4	381	100.0	381	20 AAY31740	Human CD55 and 791
5	381	100.0	381	20 AAW73505	Decay accelerating
6	361	94.8	440	8 AAP70049	Human decay accele
7	361	94.8	440	10 AAP94774	Membrane bound dec
8	361	94.8	440	16 AAR66684	Decay accelerating
9	361	94.8	440	18 AAW27483	Human glycophospha
10	323	84.8	577	17 AAW06882	Membrane co-factor

11	323	84.8	611	22 AAE12569	CAB2 protein. Uni
12	323	84.8	611	22 AAE03762	CAB-2 chimeric pro
13	323	84.8	611	22 AAE16794	CAB2 protein. Uni
14	299	78.5	299	17 AAW06881	Decay accelerating
15	296	77.7	376	20 AAY50035	Human complement r
16	296	77.7	381	18 AAW26317	Human decay accele
17	286	75.1	320	22 AAG68150	Codon modified hum
18	280	73.5	458	22 AAG75594	Human colon cancer
19	251	65.9	254	23 ABB07541	Amino acid sequenc
20	251	65.9	271	23 ABB07542	Amino acid sequenc
21	93	24.4	367	15 AAR50087	MCP:DAF fusion pro
22	65	17.1	182	21 AAB53601	Human colon cancer
23	37	9.7	37	21 AAY49760	Compact structure
24	37	9.7	37	21 AAY88076	DAF GPI anchor pep
25	37	9.7	37	21 AAY43820	Membrane anchoring
26	37	9.7	37	22 ABA45935	Transdominant effe
27	37	9.7	37	22 AAB35067	DAF membrane ancho
28	37	9.7	37	23 ABB07746	Decay accelerating
29	37	9.7	37	23 AAY76173	Decay accelerating
30	37	9.7	42	18 AAW19903	Fusion of FcRn hea
31	37	9.7	42	18 AAW19906	Fusion of beta 2-m
32	37	9.7	248	18 AAN37341	DR alpha-DAF chime
33	37	9.7	261	18 AAW37342	DR beta-1-DAF chim
34	37	9.7	272	17 AAR92254	Neural cell adhesi
35	29	7.6	29	15 AAR50086	Decay accelerating
36	23	6.0	41	20 AAY04334	Fragment of human
37	20	5.2	117	20 AAW86134	Protein sequence o
38	19	5.0	37	13 AAR20964	Sequence of decay
39	16	4.2	1006	21 AAY44455	Modified T. cruzi
40	10	2.6	10	22 AAG96997	Human complementar
41	10	2.6	10	22 AAG96999	Human complementar
42	10	2.6	10	22 AAG97001	Human complementar
43	10	2.6	10	22 AAG97003	Human complementar
44	10	2.6	10	22 AAG97005	Human complementar
45	10	2.6	10	22 AAG97007	Human complementar

ALIGNMENTS

RESULT 1	
AAAP70048	
ID	AAAP70048 standard; protein; 381 AA.
XX	
AC	AAAP70048:
XX	
DT	03-OCT-2002 (updated)
DT	03-FEB-1991 (first entry)
DE	Human decay acceleration factor variant #1.
XX	
KW	Decay acceleration factor.
XX	
OS	Homo sapiens.
XX	
FH	Key
FT	Region
FT	Location/Qualifiers
XX	331..347
XX	/label=putative transmembrane region
PN	EP244267-A.
PD	04-NOV-1987.
XX	
PF	01-MAY-1987; 87EP-0303944.
PR	02-MAY-1986; 86US-0859107.
PA	(GETH) GENENTECH INC.
XX	
PI	Carras IW.
XX	
DR	WPI; 1987-308481/44.
DR	N-PSDB; AAN70047.

XX New decay accelerating factor variants - obtained with the factor by
 PT using recombinant DNA procedures.
 XX
 XX
 PS Disclosure; Page 15-17; 20pp; English.
 XX
 CC The probable phosphatidylinositol derivatization site is Cys(330).
 CC The DAF variant is useful for treating paraoxysmal nocturnal
 CC haemoglobinuria, or inflammatory or cell lytic autoimmune
 CC diseases. It may be used to ameliorate allograft rejection
 CC or autoimmune diseases. See also AAN70046, AAN70048.
 CC (Updated on 03-OCT-2002 to add missing OS field.)
 CC
 XX
 SQ Sequence 381 AA:

Query Match 100.0%; Score 381; DB 8; Length 381;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 381; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MYVARSVAALPLLGELRRLLLVLLCPAYWGDCGLPPDVPNAOPALEGRTSPEDTV 60
 DB 1 MYVARSVAALPLLGELRRLLLVLLCPAYWGDCGLPPDVPNAOPALEGRTSPEDTV 60
 QY 61 IYKCEESFVKIPGEKDSVYCLKGSQWSDIEFCNRSCEVPRRLNSASLKOPYITQNYPP 120
 DB 61 IYKCEESFVKIPGEKDSVYCLKGSQWSDIEFCNRSCEVPRRLNSASLKOPYITQNYPP 120
 QY 121 VGTVEYECRPGYRRPRLSPKLTCLQNLKWSAVFCKKSCPNNGEIRNGIDVPGGI 180
 DB 121 VGTVEYECRPGYRRPRLSPKLTCLQNLKWSAVFCKKSCPNNGEIRNGIDVPGGI 180
 QY 181 LGATISFCNNGYKLFGSTSFCLISGSSVQWSDLPFCRELYCAPAQIDNGIIQGER 240
 DB 181 LGATISFCNNGYKLFGSTSFCLISGSSVQWSDLPFCRELYCAPAQIDNGIIQGER 240
 QY 241 DHYGYROSTYACNKGFTMIGHSIYCTVNNDEGEMSGPPPECRGKSLTSKYPPYQKPT 300
 DB 241 DHYGYROSTYACNKGFTMIGHSIYCTVNNDEGEMSGPPPECRGKSLTSKYPPYQKPT 300
 QY 301 TVNVPTEVSPTSOKTTTTPPNAQATSTPVSRTTKHFHETTPNKGSGTSGTTRLLS 360
 DB 301 TVNVPTEVSPTSOKTTTTPPNAQATSTPVSRTTKHFHETTPNKGSGTSGTTRLLS 360
 QY 361 GHTCFTLGLGLTVTMGLLT 381
 DB 361 GHTCFTLGLGLTVTMGLLT 381

RESULT 3
 AAP94773
 ID AAP94773 standard; protein; 381 AA.
 XX
 AC AAP94773;
 XX
 DT 04-JUL-1990 (first entry)
 XX
 DE Decay accelerating factor (DAF) of clones lambda 33 and lambda 47.
 XX
 KW DAF; allograft rejection; affinity purification;
 KW autoimmune disease; ds.
 XX
 OS Synthetic.
 XX
 PN W08901041-A.
 XX
 PD 09-FEB-1989.
 XX
 PF 03-AUG-1988; 88WO-US02648.
 XX
 PR 06-AUG-1987; 87US-0083757.
 XX
 PA (GETH) GENETECH INC.
 XX

PI Caras I;
 XX
 XX WPI; 1989-061177/08.
 DR N-PSDB; AAN91043.
 XX
 XX
 PT Fusion polypeptide for targeting protein to cell membrane -
 PT comprises phospholipid anchor domain with heterologous
 PT polypeptide.
 XX
 PS Disclosure; 61pp; English.
 XX
 CC Recombinant DAF's are useful in treatment of inflammatory or cell lytic
 CC autoimmune diseases and allograft rejection. Useful in diagnostic
 CC compositions or in affinity purification.
 CC
 XX
 SQ Sequence 381 AA:

Query Match 100.0%; Score 381; DB 10; Length 381;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 381; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MYVARSVAALPLLGELRRLLLVLLCPAYWGDCGLPPDVPNAOPALEGRTSPEDTV 60
 DB 1 MYVARSVAALPLLGELRRLLLVLLCPAYWGDCGLPPDVPNAOPALEGRTSPEDTV 60
 QY 61 IYKCEESFVKIPGEKDSVYCLKGSQWSDIEFCNRSCEVPRRLNSASLKOPYITQNYPP 120
 DB 61 IYKCEESFVKIPGEKDSVYCLKGSQWSDIEFCNRSCEVPRRLNSASLKOPYITQNYPP 120
 QY 121 VGTVEYECRPGYRRPRLSPKLTCLQNLKWSAVFCKKSCPNNGEIRNGIDVPGGI 180
 DB 121 VGTVEYECRPGYRRPRLSPKLTCLQNLKWSAVFCKKSCPNNGEIRNGIDVPGGI 180
 QY 181 LGATISFCNNGYKLFGSTSFCLISGSSVQWSDLPFCRELYCAPAQIDNGIIQGER 240
 DB 181 LGATISFCNNGYKLFGSTSFCLISGSSVQWSDLPFCRELYCAPAQIDNGIIQGER 240
 QY 241 DHYGYROSTYACNKGFTMIGHSIYCTVNNDEGEMSGPPPECRGKSLTSKYPPYQKPT 300
 DB 241 DHYGYROSTYACNKGFTMIGHSIYCTVNNDEGEMSGPPPECRGKSLTSKYPPYQKPT 300
 QY 301 TVNVPTEVSPTSOKTTTTPPNAQATSTPVSRTTKHFHETTPNKGSGTSGTTRLLS 360
 DB 301 TVNVPTEVSPTSOKTTTTPPNAQATSTPVSRTTKHFHETTPNKGSGTSGTTRLLS 360
 QY 361 GHTCFTLGLGLTVTMGLLT 381
 DB 361 GHTCFTLGLGLTVTMGLLT 381

RESULT 3
 AAR66683
 ID AAR66683 standard; protein; 381 AA.
 XX
 AC AAR66683;
 XX
 DT 23-JUL-1995 (first entry)
 XX
 DE Decay accelerating factor.
 XX
 KW Decay accelerating factor; DAF; mDAF; fusion protein; liposome;
 KW cell targeting; glycosphosphatidylinositol; GPI; drug delivery.
 XX
 OS Homo sapiens.
 XX
 FH Key
 FH Peptide 1..34
 FT /label= Sig_peptide
 FT Modified-site 364
 FT /note= "probable phosphatidylinositol
 FT derivatization site"
 XX
 PN US374548-A.

XX 20-DEC-1994.
XX
XX
XX 02-MAY-1986; 8605-0859107.
XX
XX 02-MAY-1986; 8605-0859107.
XX 06-AUG-1987; 8705-0083757.
XX 19-DEC-1991; 9105-0811048.
XX 12-FEB-1993; 9305-0017934.
XX
XX (GETH) GENENTECH INC.
XX
XX Caras IW;
XX
XX WPI; 1995-035649/05.
XX N-PSDB; AAQ79863.
XX
XX Liposome(s) for targeting particulate cells contg. fusion protein
XX - of glyco:phosphatidyl:inositol anchor and heterologous
XX targeting protein, e.g. for delivering toxins to infected or
XX cancer cells.
XX
XX Disclosure; Fig. 1a-1f; 36pp; English.
XX
XX A probe (given in AAQ79865) based on the N-terminal sequence of human
XX decay accelerating factor (DAF) was used to screen a HeLa cell
XX lambda cDNA library. Isolated clones encoding membrane-bound DAF
XX (MDAF) were obtained, and the full sequence of mDAF cDNA was
XX determined (AAQ79863). The GPI signal domain of mDAF may be fused to
XX a heterologous protein and targeted to cell membrane surfaces.
XX
XX Sequence 381 AA:

Query Match 100.0%; Score 381; DB 16; Length 381;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 381; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTVARPSVPAALPLGLGELPRLLLVLLCLPAVWGDCGLPPDVNPAQALGRTSFPEDTV 60
DB 1 MTVARPSVPAALPLGLGELPRLLLVLLCLPAVWGDCGLPPDVNPAQALGRTSFPEDTV 60
QY 61 IYKCESEFVKIPGEKDSVCLKGSQMSDIEFCNRSCEVPTRLNSAKOPITTONYFP 120
DB 61 IYKCESEFVKIPGEKDSVCLKGSQMSDIEFCNRSCEVPTRLNSAKOPITTONYFP 120
QY 121 VGTVEYECRPGYRREPSLSPKLTCLQNLKWSAVFCKKSCPNPEIRNGOIDVPGGI 180
DB 121 VGTVEYECRPGYRREPSLSPKLTCLQNLKWSAVFCKKSCPNPEIRNGOIDVPGGI 180
QY 181 LFGATISFSCNTGYKLGSTSFCLISGSSVQMSDPLPECREIYCPAPOIDNGIIGER 240
DB 181 LFGATISFSCNTGYKLGSTSFCLISGSSVQMSDPLPECREIYCPAPOIDNGIIGER 240
QY 241 DHYGRQSVTYACNKGFTMGESHYCTVNNDDGEMSGPPECRGSKLSJKVPYVOKPT 300
DB 241 DHYGRQSVTYACNKGFTMGESHYCTVNNDDGEMSGPPECRGSKLSJKVPYVOKPT 300
QY 301 TVNVPTEVPSIOSKTTTTPNAOATRSTPVSRTTKKHETTPNKGSGTGTMLLS 360
DB 301 TVNVPTEVPSIOSKTTTTPNAOATRSTPVSRTTKKHETTPNKGSGTGTMLLS 360
QY 361 GHRCFTLTGLGLTVMGLLT 381
DB 361 GHRCFTLTGLGLTVMGLLT 381

RESULT 4
AAQ79865
ID AAQ79865 standard; Protein; 381 AA.
AC AAQ79865;
XX
XX 22-NOV-1999 (first entry)

Applicant's
firm
Trig 10

XX Human CD55 and 791Tgp72 tumour associated antigen.
DE
XX
XX CD55; decay accelerating factor; DAF; tumour associated antigen;
KW 791Tgp72; colorectal cancer; breast cancer; ovary cancer;
KW osteosarcoma; vaccine; human.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX Peptide 1..34
XX FT /note="signal peptide"
XX FT 35..380
XX FT Protein /note="mature protein"
XX
XX WO943800-A1.
XX
XX 02-SEP-1999.
XX
XX 26-FEB-1999; 99MO-GB00582.
XX
XX 26-FEB-1999; 98GB-0004065.
XX
XX (CANC-) CANCER RES CAMPAIGN TECHNOLOGY.
XX
XX Durrant IG, Spendlove I;
XX
XX WPI; 1999-540585/45.
XX N-PSDB; AAQ87914, AAQ87915.
XX
XX Cancer vaccine containing CD55 family polypeptide, to induce at
XX least one of T helper, cytotoxic T cell or natural killer immune
XX response
XX
XX Claim 4; Fig 10; p 82pp; English.

The present sequence represents a new human tumour associated antigen, 791Tgp72, which is over-expressed on a wide range of solid tumours. The amino acid sequence of 791Tgp72 is identical to that of human CD55, although the glycosylation patterns of the 2 proteins are different. CD55 and 791Tgp72 are encoded by cDNAs (see AAQ87914 and AAQ87915) which are identical over the entire coding region, but differ in the 5' and 3' non-coding regions. A claimed cancer vaccine comprises a polypeptide of the CD55 family, including full-length CD55 or 791Tgp72, or an antigen, polypeptide, fragment or derivative of CD55 or 791Tgp72. Claimed cancer vaccines also include nucleic acids encoding CD55 or 791Tgp72 antigen, polypeptide, fragment or derivative. Claimed methods of treating a cancer patient involve administering the cancer vaccine. A method of isolating 791Tgp72 antigen from cells expressing the antigen is also claimed. The cancer vaccines induce at least one of T helper, cytotoxic T cell or natural killer immune responses, possibly also production of neutralizing antibodies and complement-mediated lysis. They are useful for treating e.g. colorectal, breast or ovarian cancer or osteosarcoma, where these are associated with overexpression of 791Tgp72.

QY Sequence 381 AA:
Best Local Similarity 100.0%; Score 381; DB 20; Length 381;
Matches 381; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTVARPSVPAALPLGLGELPRLLLVLLCLPAVWGDCGLPPDVNPAQALGRTSFPEDTV 60
DB 1 MTVARPSVPAALPLGLGELPRLLLVLLCLPAVWGDCGLPPDVNPAQALGRTSFPEDTV 60
QY 61 IYKCESEFVKIPGEKDSVCLKGSQMSDIEFCNRSCEVPTRLNSAKOPITTONYFP 120
DB 61 IYKCESEFVKIPGEKDSVCLKGSQMSDIEFCNRSCEVPTRLNSAKOPITTONYFP 120
QY 121 VGTVEYECRPGYRREPSLSPKLTCLQNLKWSAVFCKKSCPNPEIRNGOIDVPGGI 180
DB 121 VGTVEYECRPGYRREPSLSPKLTCLQNLKWSAVFCKKSCPNPEIRNGOIDVPGGI 180


```

Db 121 VGVVVEECRPGYRRRPSLSPKLTCLQNLKWSVAVEFCKKKSCPNPGEIRNGQIDVPGGI 180
QY 181 LGGATISFSCNTGKYLFGSTSSFCILISGSSVQMSDPLPECREIYCAPPQIDNGIIQGER 240
Db 181 LGGATISFSCNTGKYLFGSTSSFCILISGSSVQMSDPLPECREIYCAPPQIDNGIIQGER 240
QY 241 DHYGYROSATYACNKGFTMIGEHSTICTVNNDEGEWSGPPRCRCKSLTSKVPPTVQKPT 300
Db 241 DHYGYROSATYACNKGFTMIGEHSTICTVNNDEGEWSGPPRCRCKSLTSKVPPTVQKPT 300
QY 301 TVNVPTEVSPTSOAKTTTTPNAQATRSTPVSRTHFHETTPKKGSGTSGTTRLLS 360
Db 301 TVNVPTEVSPTSOAKTTTTPNAQATRSTPVSRTHFHETTPKKGSGTSGTTRLLS 360
QY 361 GHTCFTLTGLTGLTYMGLLT 381
Db 361 GHTCFTLTGLTGLTYMGLLT 381

RESULT 5
AAW73505
ID AAW73505 standard; Protein; 381 AA.
AC AAW73505;
DT 01-MAR-1999 (first entry)
XX
XX Decay accelerating factor protein.
DE
XX DAF; decay accelerating factor; human; compliment protein; gene therapy;
KM viral vector; ds.
XX
XX Homo sapiens.
OS
XX JP10313865-A.
PN
XX 02-DEC-1998.
PD
XX 15-MAY-1997; 97JP-0125965.
PF
XX 15-MAY-1997; 97JP-0125965.
PR
XX 15-MAY-1997; 97JP-0125965.
XX
XX (DINA-) DINABEKKU KENKYUSHO KK.
PA
XX WPT; 1999-074147/07.
DR N-PSDB; AAV08935.
XX
XX Vector having complement controlling factor - useful for gene
PT therapy
XX
XX Example 3; Page 8-9; 15pp; Japanese.
PS
XX
XX This sequence is the human decay accelerating factor (DAF) protein.
CC DAF can be used in the viral vector of the invention. The viral vector
CC contains a factor controlling the function of a human complement protein,
CC particularly a membrane combining type protein. The viral vector, which
CC is stable in situ, is useful for gene therapy.
XX
XX SQ Sequence 381 AA;

Query Match 100.0%; Score 381; DB 20; Length 381;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 381; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MTVARRSPVPAALPLGELPRLLLVLLCLPAVWGCGGLPPDVNPNQPALEGRTSPEDTV 60
Db 1 MTVARRSPVPAALPLGELPRLLLVLLCLPAVWGCGGLPPDVNPNQPALEGRTSPEDTV 60
QY 61 IITYKEESFVKIIGERKDSVYICLKGSQMSDIEFCNRSCVEPTRLNSASLQPIYITQNTFP 120
Db 61 IITYKEESFVKIIGERKDSVYICLKGSQMSDIEFCNRSCVEPTRLNSASLQPIYITQNTFP 120
QY 121 VGVVVEECRPGYRRRPSLSPKLTCLQNLKWSVAVEFCKKKSCPNPGEIRNGQIDVPGGI 180

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Db 121 VGVVVEECRPGYRRRPSLSPKLTCLQNLKWSVAVEFCKKKSCPNPGEIRNGQIDVPGGI 180
QY 181 LGGATISFSCNTGKYLFGSTSSFCILISGSSVQMSDPLPECREIYCAPPQIDNGIIQGER 240
Db 181 LGGATISFSCNTGKYLFGSTSSFCILISGSSVQMSDPLPECREIYCAPPQIDNGIIQGER 240
QY 241 DHYGYROSATYACNKGFTMIGEHSTICTVNNDEGEWSGPPRCRCKSLTSKVPPTVQKPT 300
Db 241 DHYGYROSATYACNKGFTMIGEHSTICTVNNDEGEWSGPPRCRCKSLTSKVPPTVQKPT 300
QY 301 TVNVPTEVSPTSOAKTTTTPNAQATRSTPVSRTHFHETTPKKGSGTSGTTRLLS 360
Db 301 TVNVPTEVSPTSOAKTTTTPNAQATRSTPVSRTHFHETTPKKGSGTSGTTRLLS 360
QY 361 GHTCFTLTGLTGLTYMGLLT 381
Db 361 GHTCFTLTGLTGLTYMGLLT 381

RESULT 6
AAP70049
ID AAP70049 standard; Protein; 440 AA.
AC AAP70049;
DT 03-FEB-1991 (first entry)
XX
XX Human decay acceleration factor variant #2.
DE
XX Decay acceleration factor; SDAF.
KM
XX
XX Homo sapiens.
OS
XX Key Location/Qualifiers
FH Protein 35..440
FT /label= DAF
XX
XX EP244267-A.
PN
XX 04-NOV-1987.
PD
XX
XX 01-MAY-1987; 87EP-0303944.
PF
XX 02-MAY-1986; 86US-0859107.
PR
XX (GETH ) GENENTECH INC.
PA
XX Caras IW;
PI
XX
XX WPT; 1987-308481/44.
DR N-PSDB; AAP70048.
XX
XX New decay accelerating factor variants - obtained with the factor by
PT using recombinant DNA procedures.
XX
XX Disclosure; Page 18-20; 20pp; English.
PS
XX
XX The protein sequence is a variant of decay acceleration factor, SDAF.
CC DAF and variants are useful for treating paroxysmal nocturnal
CC haemoglobinuria, or inflammatory or cell lytic autoimmune diseases.
CC They may be used to ameliorate allograft rejection or autoimmune
CC diseases.
XX See also AAP70046 and AAP70047.
XX
XX SQ Sequence 440 AA;

Query Match 94.8%; Score 361; DB 8; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 361; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MTVARRSPVPAALPLGELPRLLLVLLCLPAVWGCGGLPPDVNPNQPALEGRTSPEDTV 60

```


CC A probe (given in AA079865) based on the N-terminal sequence of human
 CC decay accelerating factor (DAF) was used to screen a HeLa cell
 CC lambda cDNA library. Isolated clones encoding soluble DAF
 CC (sDAF) were obtained; the full sequence of sDAF cDNA is given in
 CC AA079864 and the deduced protein sequence in AA06684.

XX Sequence 440 AA:

Query Match 94.8%; Score 361; DB 16; Length 440;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 361; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MTVARPSVPAALPLIGELRLILVILCLPAVWGDCGLPPDVNAPALEGRTSPEDTV 60
 DB 1 MTVARPSVPAALPLIGELRLILVILCLPAVWGDCGLPPDVNAPALEGRTSPEDTV 60
 OY 61 IYKCESEFVKIPGEKDSVYCLKGSQMSDIEFCNRSCEVPTRLNSASLKOPYITQNYFP 120
 DB 61 IYKCESEFVKIPGEKDSVYCLKGSQMSDIEFCNRSCEVPTRLNSASLKOPYITQNYFP 120
 OY 121 VGTVEYECRPGYRRPPLSPKLTCLQNLKMTAVFECKKSCPNPGEIRNGQIDVPGGI 180
 DB 121 VGTVEYECRPGYRRPPLSPKLTCLQNLKMTAVFECKKSCPNPGEIRNGQIDVPGGI 180
 OY 181 LFGATISFSCNTGYKLFGSTSFCLISGSSVQMSDPLPCRETIYCPAPQIDNGIIOGER 240
 DB 181 LFGATISFSCNTGYKLFGSTSFCLISGSSVQMSDPLPCRETIYCPAPQIDNGIIOGER 240
 OY 241 DHYGRQSVTVACNKGFTMIGEHSHIYCTVNNDEGEMSGPPRCRGSLSLTKVPTVQKPT 300
 DB 241 DHYGRQSVTVACNKGFTMIGEHSHIYCTVNNDEGEMSGPPRCRGSLSLTKVPTVQKPT 300
 OY 301 TVNVPTTEVSPTSOKTTTTPPNAQATRSPTVSKTKHFHETTPNKGSGTSGTTRLLS 360
 DB 301 TVNVPTTEVSPTSOKTTTTPPNAQATRSPTVSKTKHFHETTPNKGSGTSGTTRLLS 360
 OY 361 G 361
 DB 361 G 361

RESULT 9
 AAM27483
 ID AAM27483 standard; Protein; 440 AA.
 XX AAM27483;
 AC AAM27483;
 DE 14-APR-1998 (first entry)
 XX Human glycoposphatidylinositol anchored DAF.
 DE Human glycoposphatidylinositol anchored DAF.
 XX Human; glycoposphatidylinositol; GPI; anchored DAF; surface;
 KW homologous complement restriction factor; HCRF; medical apparatus;
 KW medical dressing; surgical equipment; diagnostic kit; prevention;
 KW purification device; reduction; complement activation.
 XX Homo sapiens.
 OS Homo sapiens.
 XX Key
 FH Location/Qualifiers
 FT 1..34
 FT Peptide /label= sig_peptide
 FT 35..440
 FT Peptide /label= mat_peptide
 PN WO9735886-A1.
 XX 02-OCT-1997.
 PD 02-OCT-1997.
 XX 12-MAR-1997; 97WO-GB00684.
 PF 12-MAR-1997; 97WO-GB00684.
 PR 31-OCT-1996; 96GB-0022694.
 PR 22-MAR-1996; 96GB-0006073.
 PR 28-MAR-1996; 96GB-0006516.

XX (IMOT-) IMOTRAN LTD.
 PA Watkins NJ;
 XX
 PI
 XX
 XX
 DR MPI: 1997-489571/45.
 DR N-PSDB: AAT90287.
 XX
 XX

PT Surfaces which prevent or reduce complement activation - having
 PT surface bound homologous complement restriction factor
 XX
 PS Example 1; Fig 1; 50pp; English.

CC The present sequence is human glycoposphatidylinositol (GPI)
 CC anchored DAF. GPI anchored DAF was used in the development of a
 CC novel surface bound to a homologous complement restriction factor
 CC (HCRF), where the surface is not a surface to which HCRF binds in
 CC vivo. The surface can be used in medical apparatus (e.g.
 CC extra-corporeal circulation systems, tubing, valves, membranes,
 CC pumps, oxygenators, catheters, cannulas, fluid reservoirs or
 CC prostheses), medical dressings, surgical equipment, diagnostic kits
 CC (e.g. kits for determining whether a patient has an abnormality
 CC which prevents the complement system from working normally or from
 CC being properly regulated) and purification devices (e.g. for
 CC purifying complement components). The surface can be used to reduce
 CC or prevent activation of complement, and to reduce morbidity due to
 CC complement activation.

XX Sequence 440 AA:

Query Match 94.8%; Score 361; DB 18; Length 440;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 361; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MTVARPSVPAALPLIGELRLILVILCLPAVWGDCGLPPDVNAPALEGRTSPEDTV 60
 DB 1 MTVARPSVPAALPLIGELRLILVILCLPAVWGDCGLPPDVNAPALEGRTSPEDTV 60
 OY 61 IYKCESEFVKIPGEKDSVYCLKGSQMSDIEFCNRSCEVPTRLNSASLKOPYITQNYFP 120
 DB 61 IYKCESEFVKIPGEKDSVYCLKGSQMSDIEFCNRSCEVPTRLNSASLKOPYITQNYFP 120
 OY 121 VGTVEYECRPGYRRPPLSPKLTCLQNLKMTAVFECKKSCPNPGEIRNGQIDVPGGI 180
 DB 121 VGTVEYECRPGYRRPPLSPKLTCLQNLKMTAVFECKKSCPNPGEIRNGQIDVPGGI 180
 OY 181 LFGATISFSCNTGYKLFGSTSFCLISGSSVQMSDPLPCRETIYCPAPQIDNGIIOGER 240
 DB 181 LFGATISFSCNTGYKLFGSTSFCLISGSSVQMSDPLPCRETIYCPAPQIDNGIIOGER 240
 OY 241 DHYGRQSVTVACNKGFTMIGEHSHIYCTVNNDEGEMSGPPRCRGSLSLTKVPTVQKPT 300
 DB 241 DHYGRQSVTVACNKGFTMIGEHSHIYCTVNNDEGEMSGPPRCRGSLSLTKVPTVQKPT 300
 OY 301 TVNVPTTEVSPTSOKTTTTPPNAQATRSPTVSKTKHFHETTPNKGSGTSGTTRLLS 360
 DB 301 TVNVPTTEVSPTSOKTTTTPPNAQATRSPTVSKTKHFHETTPNKGSGTSGTTRLLS 360
 OY 361 G 361
 DB 361 G 361

RESULT 10
 AAM06882
 ID AAM06882 standard; Protein; 577 AA.
 XX AAM06882;
 AC AAM06882;
 DE 18-MAR-1997 (first entry)
 XX Membrane co-factor protein-decay accelerating factor hybrid.
 DE Membrane co-factor protein-decay accelerating factor hybrid.
 XX

KM Complement inhibitor; membrane co-factor protein; MCP;
 KM decay accelerating factor; DAF; chimeric protein; glycosaminoglycan;
 KM heparin; cell lysis; sepsis; adult respiratory distress syndrome;
 KM reperfusion injury; cell damage.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Region 1..254
 FT /label= MCP
 FT 255..577
 FT Region /label= DAF
 XX
 PN WO634965-A2.
 XX
 PD 07-NOV-1996.
 XX
 PF 03-MAY-1996; 96MO-US06301.
 XX
 PR 05-MAY-1995; 950S-0435149.
 XX
 PA (CHIR) CHIRON CORP.
 XX
 PI Creasey AA, Innis MA, Zaror I;
 DR MPI: 1996-506167/50.
 DR N-PSDB; AAT46065.
 XX
 PT Chimeric proteins for inhibiting complement-mediated cell lysis -
 PT comprise membrane co-factor protein and decay accelerating factor
 PT peptide sequences
 XX
 PS Disclosure; Page 25-26; 33pp; English.
 XX
 CC A hybrid protein (AAM06882) comprises portions (see also AAM06880-81)
 CC of the complement-inhibitors membrane co-factor protein (MCP) and
 CC decay accelerating factor (DAF). It can be used in novel chimeric
 CC proteins also incorporating a peptide (AAM06875-79, AAM06883-90) able
 CC to bind glycosaminoglycans (esp. heparin) present on cell surfaces.
 CC The constructs are encoded by overlapping PCR (see also AAT46066-72)
 CC using MCP-DAF hybrid DNA (AAT46065) as template, and can be expressed
 CC in e.g. insect cells. The chimeric proteins are directed to cell
 CC surfaces where they inhibit complement-mediated cell lysis. They
 CC are used to treat and prevent disease states in which complement
 CC plays a role, e.g. sepsis, adult respiratory distress syndrome,
 CC reperfusion injury and tissue damage.
 CC
 XX
 SQ Sequence 577 AA:
 Query Match 84.8%; Score 323; DB 17; Length 577;
 Best Local Similarity 100.0%; Pred. No. 5.4e-298;
 Matches 323; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 35 DCGLPDPVPAQAALERTSPEDVTITTCESFVKIPKESVITLKSQMSDIEFC 94
 DB 255 DCGLPDPVPAQAALERTSPEDVTITTCESFVKIPKESVITLKSQMSDIEFC 314
 QY 95 NRSCVPTRLNSASLKOPYITTONTFPGYVVEECRPGYRREPSLSKLTCLQNLKWSA 154
 DB 315 NRSCVPTRLNSASLKOPYITTONTFPGYVVEECRPGYRREPSLSKLTCLQNLKWSA 374
 QY 155 VERCKKSCNPGEIRNGQIDVPGILFGATISFSCNTGYKLFQSTSSFCLLISGSSVQWS 214
 DB 375 VERCKKSCNPGEIRNGQIDVPGILFGATISFSCNTGYKLFQSTSSFCLLISGSSVQWS 434
 QY 215 DPLPECEITCAPAQDNLIIQGERDHYGRQSVYTAACKGFTMIEHSIYCTVNNDEG 274
 DB 435 DPLPECEITCAPAQDNLIIQGERDHYGRQSVYTAACKGFTMIEHSIYCTVNNDEG 494
 QY 275 EMSGPPRECCKSLTSKVPPTVOKPTTVNVPTEFVSPTSKTKTKTTTPNAQATRSPTVS 334
 DB 495 EMSGPPRECCKSLTSKVPPTVOKPTTVNVPTEFVSPTSKTKTKTTTPNAQATRSPTVS 554

QY 335 RTTKHFHETTPNKGSGTSGTTR 357
 DB 555 RTTKHFHETTPNKGSGTSGTTR 577
 RESULT 11
 ID AAE12569
 XX AAE12569 standard; Protein; 611 AA.
 XX
 AC AAE12569;
 XX
 DT 03-JAN-2002 (first entry)
 XX
 DE CAB2 protein.
 XX
 KM Expression vector: crippled selectable marker; neomycin resistance;
 KM HIV protein; human immunodeficiency virus; improved expression; CAB2;
 KM CAB4; amplifiable selectable marker; dihydrofolate reductase; dhfr;
 KM transgene; continuous cell line preparation.
 XX
 OS Unidentified.
 XX
 PN US2001024807-A1.
 XX
 PD 27-SEP-2001.
 XX
 PE 22-DEC-2000; 2000US-0748061.
 XX
 PR 01-NOV-1999; 99US-162930P.
 PR 30-DEC-1999; 99US-0475460.
 XX
 PA (CHIR) CHIRON CORP.
 XX
 PI Innis M, Scott EM;
 DR MPI: 2001-638503/73.
 DR N-PSDB; AAD20355.
 XX
 PT New expression vector, useful for improving expression of transgene or
 PT polypeptide, comprises 3 polynucleotides encoding crippled selectable
 PT marker, heterologous polypeptide or second amplifiable selectable
 PT marker -
 XX
 PS Example 2; Fig 1; 27pp; English.
 XX
 CC The invention relates to a new expression vector comprising a first
 CC polynucleotide encoding a first, crippled selectable marker which
 CC include sequences encoding antibiotic (neomycin) resistance containing
 CC one or more crippling mutations; second polynucleotide encoding a
 CC heterologous polypeptide of interest which is viral protein (e.g., an
 CC HIV protein) or is CAB2 or CAB4; and a third polynucleotide encoding
 CC a second amplifiable selectable marker e.g. dihydrofolate reductase
 CC (dhfr). The expression vectors are useful for the efficient expression
 CC of desired polypeptides or improving expression of a transgene of
 CC interest. The transformed cells can be used in the preparation of
 CC continuous cell lines in which the cells are essentially immortal or
 CC for the preparation of established cell lines that have the potential
 CC to be subcloned in vitro. The present sequence is CAB2 protein.
 CC Aberrant splicing of CAB2 DNA was corrected by removing donor and
 CC acceptor sites using overlapping PCR.
 CC
 XX
 SQ Sequence 611 AA:
 Query Match 84.8%; Score 323; DB 22; Length 611;
 Best Local Similarity 100.0%; Pred. No. 5.7e-298;
 Matches 323; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 35 DCGLPDPVPAQAALERTSPEDVTITTCESFVKIPKESVITLKSQMSDIEFC 94
 DB 289 DCGLPDPVPAQAALERTSPEDVTITTCESFVKIPKESVITLKSQMSDIEFC 348
 QY 95 NRSCVPTRLNSASLKOPYITTONTFPGYVVEECRPGYRREPSLSKLTCLQNLKWSA 154

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Db 349 NRSCEVPTRLNSASLKQPYITONYPFVGTVVEYECRPGYRRRPSLSPKLTCLQNLKWSYA 408
Qy 155 VEFCKKSSCPNPGELRNGQIDVPGGILFGATISFSCNTGYKILFGSTSSCLISGSSVQMS 214
Db 409 VEFCKKSSCPNPGELRNGQIDVPGGILFGATISFSCNTGYKILFGSTSSCLISGSSVQMS 468
Qy 215 DPLPECREITCPAPPOIDNGIIOGERDHYGYROSVTYACNKGFTMGEHSITCTVNNDEG 274
Db 469 DPLPECREITCPAPPOIDNGIIOGERDHYGYROSVTYACNKGFTMGEHSITCTVNNDEG 528
Qy 275 EMSGPPPECRGKSLNSKVPPTVQKPTTVNVPTEVSPTSQKTTKTTTPNAQATRSTPVS 334
Db 529 EMSGPPPECRGKSLNSKVPPTVQKPTTVNVPTEVSPTSQKTTKTTTPNAQATRSTPVS 588
Qy 335 RTTKHFHETTPNKGSGTTSQTTR 357
Db 589 RTTKHFHETTPNKGSGTTSQTTR 611

RESULT 12
AAE03762 standard; Protein; 611 AA.
AC AAE03762;
XX 07-AUG-2001 (first entry)
DE CAB-2 chimeric protein.
XX Expression vector: crippled selectable marker; CAB-2; chimeric protein;
XX heterologous polypeptide; amplifiable selectable marker;
XX viral glycoprotein; membrane cofactor protein; MCP;
XX decay accelerating factor; DAF; complement activation.
XX Unidentified.
OS WO200132901-A1.
PN 10-MAY-2001.
PD 30-DEC-1999; 99WO-US31275.
XX 01-NOV-1999; 99US-0162980.
PR (CHIR ) CHIRON CORP.
PA Innis M, Scott E;
PI WPI: 2001-389720/41.
XX N-PSDB; AAD08170.
DR Expression vectors comprising a first, crippled selectable marker and a
XX second, amplifiable selectable marker for improved production of
XX polypeptides -
PS Example 1; Fig 1; 71pp; English.
XX The present invention relates to expression vector comprising a first
XX polynucleotide encoding a first, crippled selectable marker, a second
XX polynucleotide encoding a heterologous polypeptide of interest and a
XX third polynucleotide encoding a second, amplifiable selectable marker.
XX The vector is useful for producing a polypeptide such as CAB-2, CAB-4,
XX uPAR, VEGF-D and a viral protein, especially a viral glycoprotein. The
XX expression vector solve the problems of low yield and varied expression
XX levels by using a crippled first selectable marker linked to a transgene
XX and a second, amplifiable marker, which contains a disabling mutation.
XX The tedious process of identification of high expression loci in
XX mammalian cells is eliminated and provides an efficient mechanism by
XX which any desired polypeptide can be expressed at high levels using the
XX novel cell lines generated. In addition, altering the transgene such
XX that aberrant splicing is corrected may increase expression.
XX The present sequence is CAB-2 chimeric protein that
XX combines features of membrane cofactor protein (MCP) and decay

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CC accelerating factor (DAF) to inhibit complement activation.
CC The codons in the donor sites and acceptor sites of CAB-2 DNA are
CC changed for the correction of aberrant mRNA splicing.
SQ Sequence 611 AA:
Query Match 84.8%; Score 323; DB 22; Length 611;
Best Local Similarity 100.0%; Pred. No. 5,76-298;
Matches 323; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 35 DGLPDPVNAAPALEGRTSPFEDVYITKCESFYKIPGKDSYICLKGSQMSDIEFC 94
Db 289 DGLPDPVNAAPALEGRTSPFEDVYITKCESFYKIPGKDSYICLKGSQMSDIEFC 348
Qy 95 NRSCEVPTRLNSASLKQPYITONYPFVGTVVEYECRPGYRRRPSLSPKLTCLQNLKWSYA 154
Db 349 NRSCEVPTRLNSASLKQPYITONYPFVGTVVEYECRPGYRRRPSLSPKLTCLQNLKWSYA 408
Qy 155 VEFCKKSSCPNPGELRNGQIDVPGGILFGATISFSCNTGYKILFGSTSSCLISGSSVQMS 214
Db 409 VEFCKKSSCPNPGELRNGQIDVPGGILFGATISFSCNTGYKILFGSTSSCLISGSSVQMS 468
Qy 215 DPLPECREITCPAPPOIDNGIIOGERDHYGYROSVTYACNKGFTMGEHSITCTVNNDEG 274
Db 469 DPLPECREITCPAPPOIDNGIIOGERDHYGYROSVTYACNKGFTMGEHSITCTVNNDEG 528
Qy 275 EMSGPPPECRGKSLNSKVPPTVQKPTTVNVPTEVSPTSQKTTKTTTPNAQATRSTPVS 334
Db 529 EMSGPPPECRGKSLNSKVPPTVQKPTTVNVPTEVSPTSQKTTKTTTPNAQATRSTPVS 588
Qy 335 RTTKHFHETTPNKGSGTTSQTTR 357
Db 589 RTTKHFHETTPNKGSGTTSQTTR 611

RESULT 13
AAE16794 standard; Protein; 611 AA.
ID AAE16794
XX AAE16794;
AC 09-APR-2002 (first entry)
XX CAB2 protein.
DE Expression vector: crippled selectable marker; neomycin resistance;
XX HIV protein; human immunodeficiency virus; dihydrofolate reductase;
XX CAB2; CAB4; urokinase-type plasminogen activator receptor; uPAR;
XX complement activation blocker; amplifiable selectable marker; dnfr;
XX vascular endothelial growth factor-D; VEGF-D.
XX Unidentified.
OS US6316253-B1.
PN 13-NOV-2001.
PD 30-DEC-1999; 99US-0475460.
XX 01-NOV-1999; 99US-162930P.
PR (CHIR ) CHIRON CORP.
PA Innis M, Scott EM;
PI WPI: 2002-121021/16.
XX N-PSDB; AAD27308.
DR An expression vector encoding a crippled neomycin resistance selectable
XX marker, a heterologous polypeptide and a amplifiable selectable marker.
XX useful for providing high expression of polypeptides in mammalian host
XX cells -

```

PS Example 2; Fig 1; 33pp: English.
XX
CC The invention relates to a new expression vector comprising a first
CC polynucleotide encoding a first, crippled selectable marker which
CC include sequences encoding antibiotic (neomycin) resistance containing
CC one or more crippling mutations; second polynucleotide encoding a
CC heterologous polypeptide of interest which is viral protein (e.g.
CC HIV protein) or is complement activation blocker (CAB)-2, CAB-4,
CC urokinase-type plasminogen activator receptor (uPAR) or vascular
CC endothelial growth factor-D (VEGF-D); and a third polynucleotide
CC encoding a second amplifiable selectable marker e.g. dihydrofolate
CC reductase (dhfr). The expression vector is used for stable, high
CC level expression of a polypeptide of interest in a host cell,
CC particularly mammalian cell or an insect cell. The present sequence
CC CAB2 protein. Aberrant splicing of CAB2 DNA was corrected by removing
CC donor and acceptor sites using overlapping PCR.
XX
SQ Sequence 611 AA;
Query Match 84.8%; Score 323; DB 23; Length 611;
Best Local Similarity 100.0%; Pred. No. 5.7e-298;
Matches 323; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 35 DCGLPVPVNAQPALEGRSPRETYITKCESEFVKIPGKDSVYICLKGSQMSDIEEFC 94
DB 289 DCGLPVPVNAQPALEGRSPRETYITKCESEFVKIPGKDSVYICLKGSQMSDIEEFC 348
QY 95 NRSCVEPTRLNSASIKOPYITQNFEPVGTVEYECRPGYRREPSISPRLTCLQNLKMSA 154
DB 349 NRSCVEPTRLNSASIKOPYITQNFEPVGTVEYECRPGYRREPSISPRLTCLQNLKMSA 408
QY 155 VEFCKKSCPNPGRIRNGQIDVPGILFGATISFSCNTGYALFGSTSSFCILSSSVQMS 214
DB 409 VEFCKKSCPNPGRIRNGQIDVPGILFGATISFSCNTGYALFGSTSSFCILSSSVQMS 468
QY 215 DPUPCEHETICPAPPOINDNGIIGERDHYGROSYYTAACNKGFMIGHSIYCTVNNDEG 274
DB 469 DPUPCEHETICPAPPOINDNGIIGERDHYGROSYYTAACNKGFMIGHSIYCTVNNDEG 528
QY 275 EMSGPPPCRCRKSLSKVPYVOKPTVNVPTTEVSPTSOCTTKTTTPNAQATRSTPVS 334
DB 529 EMSGPPPCRCRKSLSKVPYVOKPTVNVPTTEVSPTSOCTTKTTTPNAQATRSTPVS 588
QY 335 RTTKHFHETTPNKGSGTTSCTTR 357
DB 589 RTTKHFHETTPNKGSGTTSCTTR 611
RESULT 14
AAW06881
ID AAW06881 standard; Protein: 299 AA.
XX
AC AAW06881;
XX
DT 18-MAR-1997 (first entry)
XX
DE Decay accelerating factor.
XX
KW Complement inhibitor; membrane co-factor protein; MCP;
KW decay accelerating factor; DAF; chimeric protein; glycosaminoglycan;
KW heparin; cell lysis; sepsis; adult respiratory distress syndrome;
KW reperfusion injury; cell damage.
XX
OS Homo sapiens.
XX
PN W09634965-A2.
XX
PD 07-NOV-1996.
XX
PF 03-MAY-1996; 96MO-US06301.
XX
PR 05-MAY-1995; 95US-0435149.
XX

PA (CHIR) CHIRON CORP.
XX
PI Creasey AA, Innis MA, Zaror I;
XX
DR WPI: 1996-506167/50.
XX
PT Chimeric proteins for inhibiting complement-mediated cell lysis
PT comprise membrane co-factor protein and decay accelerating factor
PT peptide sequences
XX
PS Disclosure; Page 25; 33pp: English.
XX
XX A portion (AAW06881) of the complement-inhibitor, decay accelerating
CC factor (DAF), is used in novel chimeric proteins of formula
CC A-R1-B-R2-C, where A and C are peptides (AAW06875-79, AAW06883-90) able
CC to bind glycosaminoglycans (esp. heparin) present on cell surfaces,
CC R1 is a portion of DAF or membrane co-factor protein (MCP, see also
CC AAW06880), R2 is DAF when R1 is MCP or MCP when R1 is DAF, and B is a
CC peptide that may have complement inhibitor activity. The chimeric
CC proteins (see also AAW06882) are directed to cell surfaces where they
CC inhibit complement-mediated cell lysis. They are used to treat and
CC prevent disease states in which complement plays a role, e.g.
CC sepsis, adult respiratory distress syndrome, reperfusion injury and
CC tissue damage.
XX
SQ Sequence 299 AA;
Query Match 78.5%; Score 299; DB 17; Length 299;
Best Local Similarity 100.0%; Pred. No. 1.8e-275;
Matches 299; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 59 TVIYKCESEFVKIPGKDSVYICLKGSQMSDIEEFCNRSCVEPTRLNSASIKOPYITQNY 118
DB 1 TVIYKCESEFVKIPGKDSVYICLKGSQMSDIEEFCNRSCVEPTRLNSASIKOPYITQNY 60
QY 119 FPVGTVEYECRPGYRREPSISPRLTCLQNLKMSAVERCKKSCPNPGEIRNGQIDVPG 178
DB 61 FPVGTVEYECRPGYRREPSISPRLTCLQNLKMSAVERCKKSCPNPGEIRNGQIDVPG 120
QY 179 GILGATISFSCNTGYALFGSTSSFCILSSSVQMSDPLPCRETYICPAPPOINDNGIIG 238
DB 121 GILGATISFSCNTGYALFGSTSSFCILSSSVQMSDPLPCRETYICPAPPOINDNGIIG 180
QY 239 ERDHYGROSYYTAACNKGFMIGHSIYCTVNNDEGEMSGPPPCRCRKSLSKVPYVOK 298
DB 181 ERDHYGROSYYTAACNKGFMIGHSIYCTVNNDEGEMSGPPPCRCRKSLSKVPYVOK 240
QY 299 PTVNVPTTEVSPTSOCTTKTTTPNAQATRSTPVSRTTKHFHETTPNKGSGTTSCTTR 357
DB 241 PTVNVPTTEVSPTSOCTTKTTTPNAQATRSTPVSRTTKHFHETTPNKGSGTTSCTTR 299
RESULT 15
AAV50035
ID AAV50035 standard; Protein: 376 AA.
XX
AC AAV50035;
XX
DT 19-JAN-2000 (first entry)
XX
DE Human complement regulatory protein DAF.
XX
KW Complement regulatory protein; decay accelerating factor; DAF;
KW immune reaction; xenotransplantation; xenograft; transplant; organ;
KW rejection; hyperacute; inhibition; protection; heart; lung; liver;
KW kidney; pancreas; thyroid; islet cell; neurons; stem cell; tissue;
XX
OS Homo sapiens.
XX
PN W09953042-A2.
XX
PD 21-OCT-1999.
XX

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XX 08-APR-1999; 99MO-GB01085.
PF
XX
XX 09-APR-1998; 98GB-0007520.
PR
XX
XX (UYMA-) UNIV WALES COLLEGE OF MEDICINE.
PA
XX
XX Morgan BP, Rushmore NK, Hinchliffe SJ, Van Den Berg CW;
PI
XX WPI; 1999-620420/53.
DR
XX
XX Use of cells or tissues expressing complement regulatory molecules for,
PT e.g. preventing xenotransplant rejection in humans
PT
XX
XX Claim 18; Fig 15; 88pp; English.
PS
XX
XX This sequence represents human complement regulatory protein DAF
CC (decay accelerating factor). Complement regulatory proteins (CRPs)
CC such as DAF and CD59 are membrane bound proteins that protect an
CC organism's cells from attack by its own complement. Hyperacute
CC rejection of a xenotransplant occurs because natural antibodies in
CC the human recipient bind to the endothelium of the donor organ and
CC activate complement, thereby initiating rapid rejection.
CC Hyperexpression of this protein in pig cells may be useful for the
CC protection of xenotransplanted organs, as greatly increased amounts
CC of functional CRP molecules will be expressed. The organ should be
CC resistant to attack by human complement, thus preventing organ
CC rejection. Methods of causing donor animal cells to hyperexpress CRPs
CC can be used for protection of xenotransplants. For example, organs,
CC tissue and cells can be generated which are resistant to complement
CC attack and hence to hyperacute rejection when transplanted into humans.
CC The methods can be used for organs, such as heart, lung, liver, kidney,
CC pancreas and thyroid; cells, such as islet cells, neurons, and stem
CC cells; or tissues, such as skin.
XX
SQ Sequence 376 AA:
Query Match 77.7%; Score 296; DB 20; Length 376;
Best Local Similarity 100.0%; Pred. No. 1.6e-272;
Matches 296; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 86 QMSDIEFCRSCSEVPTRLNSASLKOPIYTONFEPVGVVEYECRPGYRREPSISPLTLC 145
DB 81 QMSDIEFCRSCSEVPTRLNSASLKOPIYTONFEPVGVVEYECRPGYRREPSISPLTLC 140
OY 146 LQNLKMWSTAVEFCRCKKSCPNPGEIRNGQIDVPGCILFGATISFSCNTGYKLFGSTSFCFL 205
DB 141 LQNLKMWSTAVEFCRCKKSCPNPGEIRNGQIDVPGCILFGATISFSCNTGYKLFGSTSFCFL 200
OY 206 ISSSSVQMSDPLPECREIYCPAPQIDNGIIOGERDHYGROSVTYACNKGFTMIGEHST 265
DB 201 ISSSSVQMSDPLPECREIYCPAPQIDNGIIOGERDHYGROSVTYACNKGFTMIGEHST 260
OY 266 YCTVNNDEGEMSGPPECRCKSLTSKYVPTVOKPTTVNPTTEVSPTSOKTTKTTTPNA 325
DB 261 YCTVNNDEGEMSGPPECRCKSLTSKYVPTVOKPTTVNPTTEVSPTSOKTTKTTTPNA 320
OY 326 QATRTSTPVASRTTKHFHETTPNKGSGTTSCTTRLLSGHTCFTLLGLGLTVMGLLT 381
DB 321 QATRTSTPVASRTTKHFHETTPNKGSGTTSCTTRLLSGHTCFTLLGLGLTVMGLLT 376
```

Search completed: February 12, 2003, 11:10:26
Job time : 40 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: February 12, 2003, 11:09:26 ; Search time 22 Seconds
(without alignments)
1664.873 Million cell updates/sec

Title: US-09-623-035-2
Perfect score: 381
Sequence: 1 MVARPSVPAALPLGLRPR.....HTCFTLNGLLGLVTWGLLT 381

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 283224 seqs, 96134422 residues
Word size : 0

Total number of hits satisfying chosen parameters: 283224
Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	381	100.0	381	1 B26359	decay-accelerating
2	361	94.8	440	2 A26359	decay-accelerating
3	85	22.3	340	2 I56234	decay-accelerating
4	9	2.4	345	1 NBHU	apolipoprotein H p
5	9	2.4	2470	2 I50726	cation-independent
6	8	2.1	307	2 D83295	transaldolase PA27
7	8	2.1	347	2 G75283	asparaginase (EC 3
8	8	2.1	413	2 H75628	hypothetical prote
9	8	2.1	426	2 A10287	conserved hypotnet
10	8	2.1	503	2 A49432	activin receptor-1
11	8	2.1	555	2 T44010	virion protein (im
12	8	2.1	558	2 S57953	CABP protein alpha
13	7	1.8	42	2 A37896	progesterone recep
14	7	1.8	98	2 AE2201	hypothetical prote
15	7	1.8	106	2 AD0408	conserved hypotnet
16	7	1.8	115	2 AC1134	hypothetical prote
17	7	1.8	131	2 T22997	hypothetical prote
18	7	1.8	143	2 S47832	hypothetical 15.6K
19	7	1.8	143	2 A98190	hypothetical prote
20	7	1.8	143	2 B86037	hypothetical prote
21	7	1.8	147	2 S57440	hypothetical prote
22	7	1.8	156	1 NNHU1	lydb protein - pha
23	7	1.8	192	2 AH3643	pancreatic ribonuc
24	7	1.8	204	2 S52644	cytochrome b561 [i
25	7	1.8	211	2 A46458	phycobilisome matu
26	7	1.8	212	2 A81190	human CRI homolog
27	7	1.8	212	2 G81913	conserved hypotnet
28	7	1.8	219	2 A10886	hypothetical prote
29	7	1.8	222	2 AC2397	Deda-family integr
					ATP-binding protei

30	7	1.8	224	2 D83570	probable nucleotid
31	7	1.8	232	2 A82426	myoglobin ABC tra
32	7	1.8	243	2 S25755	Ig lambda chain -
33	7	1.8	243	2 A70670	hypothetical prote
34	7	1.8	261	2 B69095	covalt transport m
35	7	1.8	269	2 F8662	phosphonate ABC tr
36	7	1.8	272	2 G71618	merozoite surface
37	7	1.8	275	2 G69963	lipoprotein SpoIII
38	7	1.8	276	2 G64584	conserved hypotnet
39	7	1.8	283	2 B87546	acetoin dehydrogen
40	7	1.8	284	2 S27843	homeotic protein s
41	7	1.8	286	2 S08993	signal sequence re
42	7	1.8	286	2 I38246	signal sequence re
43	7	1.8	289	2 AD1354	oxidoreductase hom
44	7	1.8	291	2 A55980	opsin-related reti
45	7	1.8	291	2 I46965	G protein-coupled

ALIGNMENTS

RESULT 1
B26359
decay-accelerating factor, GPI-anchored splice form precursor - human
N:Alternate names: CD55; DAF splice form 2; decay-accelerating factor membrane-bound
C:Species: Homo sapiens (man)
C>Date: 05-Oct-1988 #sequence revision 16-Aug-1996 #text-change 19-Jan-2001
C:Accession: B26359; A27666; A39101; I52564; I52564
R:Caras, I.W.; Davitz, M.A.; Rhee, L.; Weddell, G.; Martin Jr., D.W.; Nussenzweig, V.
Nature 325, 545-549, 1987
A:Title: Cloning of decay-accelerating factor suggests novel use of splicing to gener
A:Reference number: A26359; MUID:87115845; PMID:2433596
A:Accession: B26359
A:Molecule type: mRNA
A:Residues: 1-381 <CAR>
A:Cross-references: GB:M50142; NID:g181464; PIDN:AAA52168.1; PID:g181465
R:Medoff, M.E.; Lublin, D.M.; Holers, V.M.; Ayers, D.J.; Getty, R.R.; Leykam, J.F.; At
Proc. Natl. Acad. Sci. U.S.A. 84, 2007-2011, 1987
A:Title: Cloning and characterization of cDNAs encoding the complete sequence of deca
A:Reference number: A27666; MUID:87175602; PMID:2436222
A:Accession: A27666
A:Molecule type: mRNA
A:Residues: 6-79, 'T', '81-84, 'M', '86-381 <MED>
A:Cross-references: GB:M57939; NID:g181462; PIDN:AAA52167.1; PID:g181463
R:Moran, P.; Raab, H.; Kohr, W.J.; Caras, I.W.
J. Biol. Chem. 266, 1250-1257, 1991
A:Title: Glycophospholipid membrane anchor attachment. Molecular analysis of the clea
A:Reference number: A39101; MUID:91093238; PMID:1824699
A:Accession: A39101
A:Molecule type: protein
A:Residues: 338-352 <MOR>
R:Lublin, D.M.; Mallinson, G.; Poole, J.; Reid, M.E.; Thompson, E.S.; Ferdman, B.R.;
Blood 84, 1276-1282, 1994
A:Title: Molecular basis of reduced or absent expression of decay-accelerating factor
A:Reference number: I52594; MUID:94325573; PMID:7519480
A:Accession: I52594
A>Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 194-198, 'U', '200-209 <LUB>
A:Cross-references: GB:S72858; NID:g639599; PIDN:AAC60633.1; PID:g639600
A:Experimental source: Individual KW, Cromer blood group phenotype Dr(a-)
A:Note: the single nucleotide difference in this allele, which changes Ser-199 to Leu
on (see reference I52564), and thus reduced DAF expression
R:Reid, M.E.; Mallinson, G.; Slim, R.B.; Poole, J.; Pausch, V.; Merry, A.H.; Llew, Y.W
Blood 78, 3591-3297, 1991
A:Title: Biochemical studies on red blood cells from a patient with the Inab phenotyp
A:Reference number: I52564; MUID:92075980; PMID:1720702
A:Accession: I52564
A>Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 190-193, 'Q' <CPVE>
A:Cross-references: GB:S70668; NID:g240301; PIDN:AMB20576.1; PID:g240302
A:Experimental source: Individual KW, Cromer blood group phenotype Dr(a-) (described

C:Comment: Cromer blood group system antigens reside on this protein.
 C:Comment: For an alternative splice form, see PIR:A26359.
 C:Genetics:
 A:Gene: GDB:DAF
 A:Cross-references: GDB:119088; OMIM:125240
 A:Map position: 1q32-1q32
 C:Function:
 A:Description: protects tissues from damage by regulating complement activation on cell
 A:Superfamily: decay-accelerating factor; complement factor H repeat homology
 C:Keywords: alternative splicing; blocked carboxyl end; complement inhibitor; glycoprotein
 F:1-34/Domain: signal sequence #status predicted <SIG>
 F:35-33/Product: decay-accelerating factor 2 #status predicted <MAN>
 F:35-94/Domain: complement factor H repeat homology <FH01>
 F:98-158/Domain: complement factor H repeat homology <FH02>
 F:163-220/Domain: complement factor H repeat homology <FH03>
 F:225-283/Domain: complement factor H repeat homology <FH04>
 F:354-381/Domain: carboxyl-terminal propeptide #status predicted <PRO>
 F:95/Binding site: carbohydrate (Asn) (covalent) #status predicted
 F:353/Modified site: GPI-anchor ethanolamine amidated carboxyl end (Ser) (in mature form)

Query Match 100.0% Score 381; DB 1; Length 381;
 Best Local Similarity 100.0%; Pred. No. 0; Mismatches 0; Indels 0; Gaps 0;
 Matches 381; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTVARPSVPALPLGLPRLILVLLCLPAVWGDCGLPPDVPAQALRGRTSPEDTY 60
 Db 1 MTVARPSVPALPLGLPRLILVLLCLPAVWGDCGLPPDVPAQALRGRTSPEDTY 60
 QY 61 IYKCESFVKIPGEKDSVLCCKGSDIEFCNRCSEVPTRLNSALSKQPYITQNYFP 120
 Db 61 IYKCESFVKIPGEKDSVLCCKGSDIEFCNRCSEVPTRLNSALSKQPYITQNYFP 120
 QY 121 VGVVVEECRPGYRREPSLSPKLTCLQNLKMTAVCECKKSCPNGEIRNGQIDVPGGI 180
 Db 121 VGVVVEECRPGYRREPSLSPKLTCLQNLKMTAVCECKKSCPNGEIRNGQIDVPGGI 180
 QY 181 LFGATISFSCNTGKFLGSGTSSFCILSGSSVQSDPLPECREIYCPAPPOINDGIIIGER 240
 Db 181 LFGATISFSCNTGKFLGSGTSSFCILSGSSVQSDPLPECREIYCPAPPOINDGIIIGER 240
 QY 241 DHGYSQSVTYACNKGFTMIGHSIYCTVNNDEGMSGPPRECKGSLTSKVPYVQKPT 300
 Db 241 DHGYSQSVTYACNKGFTMIGHSIYCTVNNDEGMSGPPRECKGSLTSKVPYVQKPT 300
 QY 301 TVVAVPTTEVSPTSOQKTTTKTTPNAQATRSTPVSRTHKHETTPNKGSGTSTGTRLLS 360
 Db 301 TVVAVPTTEVSPTSOQKTTTKTTPNAQATRSTPVSRTHKHETTPNKGSGTSTGTRLLS 360
 QY 361 GHTCFITLGLGLTVMGLLT 381
 Db 361 GHTCFITLGLGLTVMGLLT 381

RESULT 2
 A26359
 decay-accelerating factor, splice form 1 precursor - human
 N:Alternate names: decay-accelerating factor 5; decay-accelerating factor secreted form
 C:Species: Homo sapiens (man)
 C>Date: 05-Oct-1988 #sequence, revision 05-Oct-1988 #text, change 02-Jun-2000
 C:Accession: A26359; A39702; S16187; S23138; A27258
 R:Carls, I.W.; Davitz, M.A.; Rhee, L.; Weddell, G.; Martin Jr., D.W.; Nussenzweig, V.
 Nature 335, 545-549, 1987
 A:Title: Cloning of decay-accelerating factor suggests novel use of splicing to generate
 A:Reference number: A26359; MUID:87115845; PMID:2433596
 A:Accession: A26359
 A:Molecule type: mRNA
 A:Residues: 1-440 <CRNA>
 A:Cross-references: GB:M30142
 R:Emilioni, U.K.; Ravi, L.; Medof, M.E.
 Proc. Natl. Acad. Sci. U.S.A. 88, 4675-4679, 1991
 A:Title: Characterization of the decay-accelerating factor gene promoter region.
 A:Reference number: A39702; MUID:91271256; PMID:1711208
 A:Accession: A39702

A:Molecule type: DNA
 A:Residues: 1-79, 'T', 81-104 <EMD>
 A:Cross-references: GB:M64356
 A:Note: the authors translated the codon AGT for residue 85 as Met
 R:Nakano, Y.; Sugita, Y.; Ishikawa, Y.; Choi, N.H.; Tobe, T.; Tomita, M.
 Biochim. Biophys. Acta 1074, 326-330, 1991
 A:Title: Isolation of two forms of decay-accelerating factor (DAF) from human urine.
 A:Reference number: S16187; MUID:91291869; PMID:1712233
 A:Accession: S16187
 A>Status: preliminary
 A:Molecule type: protein
 A:Residues: 35-47 <BIO>
 R:Nakano, Y.; Sunida, K.; Kikuta, N.; Miura, N.H.; Tobe, T.; Tomita, M.
 Biochim. Biophys. Acta 1116, 235-240, 1992
 A:Title: Complete determination of disulfide bonds localized within the short consens
 A:Reference number: S23138; MUID:92305034; PMID:1377029
 A:Accession: S23138
 A>Status: preliminary
 A:Molecule type: protein
 A:Residues: 35-41, 65-68, 79-81, 93-103, 128-134, 143-145, 155-159, 162-168, 188-192, 203-204;
 R:Sugita, Y.; Negoro, T.; Matsuda, T.; Sakamoto, T.; Tomita, M.
 J. Biochem. 100, 143-150, 1986
 A:Title: Improved method for the isolation and preliminary characterization of human
 A:Reference number: A27258; MUID:87008461; PMID:2428813
 A:Accession: A27258
 A:Molecule type: protein
 A:Residues: 35, 'X', '37', 'G', '39-51', 'P', '53-55', 'X', '57-58', 'X', '60-63 <SUG>
 A:Note: gly-35 and leu-38 were also found
 C:Comment: For an alternative splice form, see PIR:B26359
 C:Genetics:
 A:Gene: GDB:DAF
 A:Cross-references: GDB:119088; OMIM:125240
 A:Map position: 1q32-1q32
 C:Superfamily: decay-accelerating factor; complement factor H repeat homology
 C:Keywords: alternative splicing; glycoprotein
 F:1-34/Domain: signal sequence #status predicted <SIG>
 F:35-44/Product: decay-accelerating factor 1 #status predicted <MAN>
 F:36-94/Domain: complement factor H repeat homology <FH01>
 F:98-158/Domain: complement factor H repeat homology <FH02>
 F:163-220/Domain: complement factor H repeat homology <FH03>
 F:225-283/Domain: complement factor H repeat homology <FH04>
 F:95/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 94.8% Score 361; DB 2; Length 440;
 Best Local Similarity 100.0%; Pred. No. 0; Mismatches 0; Indels 0; Gaps 0;
 Matches 361; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTVARPSVPALPLGLPRLILVLLCLPAVWGDCGLPPDVPAQALRGRTSPEDTY 60
 Db 1 MTVARPSVPALPLGLPRLILVLLCLPAVWGDCGLPPDVPAQALRGRTSPEDTY 60
 QY 61 IYKCESFVKIPGEKDSVLCCKGSDIEFCNRCSEVPTRLNSALSKQPYITQNYFP 120
 Db 61 IYKCESFVKIPGEKDSVLCCKGSDIEFCNRCSEVPTRLNSALSKQPYITQNYFP 120
 QY 121 VGVVVEECRPGYRREPSLSPKLTCLQNLKMTAVCECKKSCPNGEIRNGQIDVPGGI 180
 Db 121 VGVVVEECRPGYRREPSLSPKLTCLQNLKMTAVCECKKSCPNGEIRNGQIDVPGGI 180
 QY 181 LFGATISFSCNTGKFLGSGTSSFCILSGSSVQSDPLPECREIYCPAPPOINDGIIIGER 240
 Db 181 LFGATISFSCNTGKFLGSGTSSFCILSGSSVQSDPLPECREIYCPAPPOINDGIIIGER 240
 QY 241 DHGYSQSVTYACNKGFTMIGHSIYCTVNNDEGMSGPPRECKGSLTSKVPYVQKPT 300
 Db 241 DHGYSQSVTYACNKGFTMIGHSIYCTVNNDEGMSGPPRECKGSLTSKVPYVQKPT 300
 QY 301 TVVAVPTTEVSPTSOQKTTTKTTPNAQATRSTPVSRTHKHETTPNKGSGTSTGTRLLS 360
 Db 301 TVVAVPTTEVSPTSOQKTTTKTTPNAQATRSTPVSRTHKHETTPNKGSGTSTGTRLLS 360
 QY 361 G 361

Db 361 G 361

RESULT 3

156234
decay-accelerating factor - orangutan (fragment)
C:Species: Pongo pygmaeus (orangutan)
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 20-Aug-1999
C:Accession: 156234
R:Nickells, M.W.; Alvarez, J.I.; Lublin, D.M.; Atkinson, J.P.
J. Immunol. 152, 676-685, 1994
A:Title: Characterization of DAF-2, a high molecular weight form of decay-accelerating factor
A:Reference number: 156234; MUID:94110622; PMID:7506731
A:Accession: 156234
A:Status: preliminary; translated from GR/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-340 <RES>
A:Cross-references: GB:567775; NID:g459389; PIDN:AMC0609.1; PID:g459390
C:Superfamily: decay-accelerating factor; complement factor H repeat homology
F:1-53/Domain: complement factor H repeat homology (fragment) <FH01>
F:57-117/Domain: complement factor H repeat homology <FH02>
F:122-119/Domain: complement factor H repeat homology <FH03>
F:164-242/Domain: complement factor H repeat homology <FH04>

Query Match 22.3%; Score 85; DB 2; Length 340;
Best Local Similarity 100.0%; Pred. No. 5.4e-76;
Matches 85; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 272 DEGEWGGPPPCRGKSLTSKVPYQKRTYVNPPTTEVSPTSQKTTTTPNMAQTST 331

Db 231 DEGEWGGPPPCRGKSLTSKVPYQKRTYVNPPTTEVSPTSQKTTTTPNMAQTST 290

Qy 332 PVSRTTKHFHETTPKNGSGTSGTT 356

Db 291 PVSRTTKHFHETTPKNGSGTSGTT 315

RESULT 4

NBHU

apolipoprotein H precursor [validated] - human
N:Alternate names: activated protein C-binding protein; antidiolipin cofactor; beta-2
C:Species: Homo sapiens (man)
C:Date: 17-May-1995 #sequence_revision 30-Jun-1993 #text_change 08-Dec-2000
C:Accession: S17178; S17668; J01379; B43286; A03209; A46464; I54745; S15499; S20
R:Steinmasser, A.; Estallier, C.; Weiss, E.H.; Sim, R.B.; Day, A.J.
Biochem. J. 277, 387-391, 1991
A:Title: Complete nucleotide and deduced amino acid sequence of human beta(2)-glycoprote
A:Reference number: S17178; MUID:91315408; PMID:1650181
A:Accession: S17668
A:Molecule type: mRNA
A:Residues: 1-345 <STP>
A:Cross-references: EMBL:X58100; NID:g28809; PIDN:CAA41113.1; PID:g28810
R:Kristensen, T.; Schousboe, I.; Boel, E.; Mulvihill, E.M.; Rosendahl Hansen, R.; Bach M
FEBS Lett. 289, 183-186, 1991
A:Title: Molecular cloning and mammalian expression of human beta(2)-glycoprotein I cDNA
A:Reference number: S17668; MUID:92008618; PMID:1655523
A:Accession: S17668
A:Molecule type: mRNA
A:Residues: 1-345 <KKRI>
A:Cross-references: EMBL:X53595; NID:g28811; PIDN:CAA37664.1; PID:g28812
R:Mehdi, H.; Nunn, M.; Steel, D.M.; Whitehead, A.S.; Perez, M.; Walker, L.; Peeples, M.E
Gene 108, 293-298, 1991
A:Title: Nucleotide sequence and expression of the human gene encoding apolipoprotein H
A:Reference number: J01379; MUID:92084151; PMID:1748314
A:Accession: J01379
A:Molecule type: mRNA
A:Residues: 1-265, 'V', 267-345 <MEH>
A:Cross-references: EMBL:X57847; NID:g28813; PIDN:CAA40977.1; PID:g28814
R:Nonaka, M.; Matsuda, Y.; Shiroishi, T.; Motiwaki, K.; Nonaka, M.; Natsume-Sakai, S.
Genomics 13, 1082-1087, 1992
A:Title: Molecular cloning of mouse beta-2-glycoprotein I and mapping of the gene to chr
A:Reference number: A43286; MUID:92372000; PMID:1339387

A:Accession: B43286
A:Status: not compared with conceptual translation

A:Molecule type: mRNA

A:Residues: 1-265, 'V', 267-345 <NON>

R:Lozier, J.; Takahashi, N.; Putnam, F.W.
Proc. Natl. Acad. Sci. U.S.A. 81, 3640-3644, 1984

A:Title: Complete amino acid sequence of human plasma beta2-glycoprotein I.

A:Reference number: A03209; MUID:84222015; PMID:6587378

A:Accession: A03209

A:Molecule type: protein

A:Residues: 20-120, 'C', 122-187, 'N', 189-265, 'V', 267-345 <LOZ>

R:McNell, H.P.; Simpson, R.J.; Chesterman, C.N.; Killis, S.A.
Proc. Natl. Acad. Sci. U.S.A. 87, 4120-4124, 1990

A:Title: Anti-phospholipid antibodies are directed against a complex antigen that inc

A:Reference number: A35786; MUID:90272666; PMID:2349221

A:Accession: A35786

A:Molecule type: protein

A:Residues: 20-22, 'X', 24-37, 'X', 39-43 <MCN>

R:Matsura, E.; Igarashi, Y.; Fujimoto, M.; Ichikawa, K.; Suzuki, T.; Sumida, T.; Yas
J. Immunol. 148, 3885-3891, 1992

A:Title: Heterogeneity of antidiolipin antibodies defined by the antidiolipin c

A:Reference number: A46464; MUID:92291509; PMID:1602135

A:Accession: A46464

A:Molecule type: protein

A:Residues: 20-44 <MA2>

A:Note: sequence extracted from NCBI backbone (NCBI:105524)
R:Matsura, E.; Igarashi, M.; Igarashi, Y.; Nage, H.; Ichikawa, K.; Yasuda, T.; Kolk
Int. Immunol. 3, 1217-1221, 1991

A:Title: Molecular definition of human beta 2-glycoprotein I (beta 2-GPI) by cDNA clo

A:Reference number: I54745; MUID:92135065; PMID:1777418

A:Accession: I54745

A:Status: preliminary; translated from GR/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-265, 'V', 267-345 <RES>

A:Cross-references: GB:S80305; NID:g244677; PIDN:ABR21330.1; PID:g244678

C:Comment: This plasma glycoprotein is a constituent of chylomicrons, VLDL, and HDL.
sic blood coagulation cascade and ADP-mediated platelet aggregation.

C:Comment: The physiological role of this protein is uncertain. It may diminish unwar

C:Genetics:

A:Gene: GDB:AP0H

A:Cross-references: GDB:118887; OMIM:138700

A:Map position: 19q23-17qter

C:Superfamily: apolipoprotein H; complement factor H repeat homology

C:Keywords: chylomicron; duplication; glycoprotein; HDL; heparin binding; lipid bindi

F:1-19/Domain: signal sequence #status predicted <SIG>

F:20-345/Product: apolipoprotein H #status experimental <MAT>

F:84-137/Domain: complement factor H repeat homology <FH1>

F:142-200/Domain: complement factor H repeat homology <FH3>

F:205-260/Domain: complement factor H repeat homology <FH4>

F:264-325/Domain: complement factor H repeat homology <FH5>

F:23-66, 51-79, 110-137, 174-200, 205-248, 300-307/Disulfide bonds: #status experimental

F:84-124, 142-188, 234-260, 264-315, 335-345/Disulfide bonds: #status predicted

F:162, 183, 193, 253/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match 2.4%; Score 9; DB 1; Length 345;
Best Local Similarity 100.0%; Pred. No. 1.2;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 185 TISFSCNTG 193

Db 105 TISFSCNTG 113

RESULT 5

150726

cation-independent mannose-6-phosphate receptor - chicken

C:Species: Gallus gallus (chicken)

C:Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 20-Aug-1999

C:Accession: I50726

R:Zhou, M.; Ma, Z.; Sly, W.S.
Proc. Natl. Acad. Sci. U.S.A. 92, 9762-9766, 1995

A:Title: Cloning and expression of the cDNA of chicken cation-independent mannose-6-p

A:Reference number: I50726; MUID:96003859; PMID:7568213
A:Accession: I50726
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-2470 <RH0>
A:Cross-references: EMBL:U55037; NID:91019118; PIDN:AAC59718.1; PID:91019119
C:Superfamily: mannose 6-phosphate receptor, cation-independent; fibronectin type II ref F:1882-1921/Domain: fibronectin type II repeat homology <2F1>

Query Match 2.4%; Score 9; DB 2; Length 2470;
Best Local Similarity 100.0%; Pred. No. 6.6;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 22 LLLVLLCLP 30
Db 9 LLLVLLCLP 17

RESULT 6

D83295
transaldolase PA2796 [imported] - Pseudomonas aeruginosa (strain PA01)
C:Species: Pseudomonas aeruginosa
C>Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C:Accession: D83295
R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; Br
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,
.; Lory, S.; Olson, M.V.
A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho
A:Reference number: A82950; MUID:20437337; PMID:10984043
A:Accession: D83295
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-307 <ST0>
A:Cross-references: GB:AE004707; GB:AE004091; NID:99948876; PIDN:AAG06184.1; GSPDB:GN001
A:Experimental source: strain PA01
C:Genetics:
A:Gene: tal; PA2796
C:Superfamily: human transaldolase

Query Match 2.1%; Score 8; DB 2; Length 307;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 GELPRLLL 23
Db 249 GELPRLLL 256

RESULT 7

G75283
asparaginase (EC 3.5.1.1) [similarity] - Deinococcus radiodurans (strain R1)
C:Species: Deinococcus radiodurans
C>Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 21-Jul-2000
C:Accession: G75283
R:White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;
S.; Smith, H.O.; Venter, J.C.; Lam, P.; McDonald, L.; Uterback, T.; Zalewski, C.; Ma
Science 286, 1571-1577, 1999
A:Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
A:Reference number: A75250; MUID:20036896; PMID:10567266
A:Accession: G75283
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-347 <WH1>
A:Cross-references: GB:AE002066; GB:AE000513; NID:96460163; PIDN:AAF11899.1; PID:9646016
A:Experimental source: strain R1
C:Genetics:
A:Gene: DR2353
A:Map position: 1
C:Superfamily: asparaginase
C:Keywords: hydrolase

Query Match 2.1%; Score 8; DB 2; Length 347;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 20 RLLLVLL 27
Db 322 RLLLVLL 329

RESULT 8

H75628
hypothetical protein - Deinococcus radiodurans (strain R1)
C:Species: Deinococcus radiodurans
C>Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 31-Mar-2000
C:Accession: H75628
R:White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J
.; M.; Shen, M.; Yamathayan, J.J.; Lam, P.; McDonald, L.; Uterback, T.; Zalewski, C.;
S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
A:Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
A:Reference number: A75250; MUID:20036896; PMID:10567266
A:Accession: H75628
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-413 <WH1>
A:Cross-references: GB:AE001826; NID:96460827; PIDN:AAF12617.1; PID:96460913; TIGR:DR
A:Experimental source: strain R1
C:Genetics:
A:Gene: DRB0098
A:Map position: megaplasmid
A:Genome: plasmid
A:Note: plasmid MPI

Query Match 2.1%; Score 8; DB 2; Length 413;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 LPLIGELP 19
Db 27 LPLIGELP 34

RESULT 9

AI0287
conserved hypothetical protein YPO2360 [imported] - Yersinia pestis (strain CO92)
C:Species: Yersinia pestis
C>Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Nov-2001
C:Accession: AI0287
R:Parkhill, J.; Wren, B.W.; Thomson, N.R.; Tlball, R.W.; Holden, M.T.G.; Prentice, M
deno-farraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G
11, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrel
Nature 413, 523-527, 2001
A:Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A:Reference number: AB0001; MUID:21470413; PMID:11586360
A:Accession: AI0287
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-426 <YUR>
A:Cross-references: GB:AL590842; PIDN:CAC91165.1; PID:915980357; GSPDB:GN00175
C:Genetics:
A:Gene: YPO2360
C:Superfamily: Escherichia coli probable membrane protein yciW

Query Match 2.1%; Score 8; DB 2; Length 426;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 300 TTVNVPTT 307
Db 34 TTVNVPTT 41

RESULT 10

A49432
 activin receptor-like kinase 5 precursor - human
 C:Accession: S57953
 R:Hillard, A.; Thern, A.; Dahlback, B.
 submitted to the EMBL Data Library, July 1995
 A:Description: Molecular cloning of rat C4b-binding protein alpha- and beta-chains: s
 A:Reference number: S57953
 A:Accession: S57953
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-558 <HLI>
 A:Cross-references: EMBL:Z50051; NID:9899379; PIDN:CA930391.1; PID:9899380
 C:Superfamily: C4b-binding protein alpha chain; complement factor H repeat homology
 F:15-72/Domain: complement factor H repeat homology <FH1>
 F:77-134/Domain: complement factor H repeat homology <FH2>
 F:139-199/Domain: complement factor H repeat homology <FH3>
 F:204-258/Domain: complement factor H repeat homology <FH4>
 F:263-324/Domain: complement factor H repeat homology <FH5>
 F:328-386/Domain: complement factor H repeat homology <FH6>
 F:390-443/Domain: complement factor H repeat homology <FH7>
 F:447-501/Domain: complement factor H repeat homology <FH8>

Query Match 2.1%; Score 8; DB 2; Length 503;
 Best Local Similarity 100.0%; Pred. No. 16;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 19 PRLTLVL 26
 |||||
 Db 10 PRLTLVL 17

RESULT 11
 T44010
 varion protein [imported] - human herpesvirus 6
 C:Species: human herpesvirus 6
 C:Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 21-Jul-2000
 C:Accession: T44010; T44197
 R:Isegawa, Y.; Mukai, T.; Nakano, K.; Kagawa, M.; Chen, J.; Mori, Y.; Sunagawa, T.; Kaw
 J. VIOL. 73, 8053-8063, 1999
 A:Title: Comparison of the complete DNA sequences of human herpesvirus 6 variants A and
 A:Reference number: 222732; MUID:99412319; PMID:10482554
 A:Accession: T44010
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-555 <ISE>
 A:Cross-references: EMBL:AB021506; NID:9495977; PIDN:BA78271.1; PID:9496038
 A:Experimental source: strain HST; pop. variant B
 R:Dominguez, G.; Damhaugh, T.R.; Stamey, F.R.; Dewhurst, S.; Inoue, N.; Pellett, P.E.
 J. VIOL. 73, 8040-8052, 1999
 A:Title: Human herpesvirus 6B genome sequence: coding content and comparison with human
 A:Reference number: 222734; MUID:99412318; PMID:10482553
 A:Accession: T44197
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-555 <DOM>
 A:Cross-references: EMBL:AF157706; PIDN:AAB06348.1
 A:Experimental source: strain 229; variant B
 C:Genetics:
 A:Gene: US0
 C:Superfamily: varicella-zoster virus gene 34 protein

Query Match 2.1%; Score 8; DB 2; Length 555;
 Best Local Similarity 100.0%; Pred. No. 18;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 71 KIPGEKDS 78
 |||||
 Db 311 KIPGEKDS 318

RESULT 12
 S57953
 C4BP protein alpha chain precursor - rat
 C:Species: Rattus norvegicus (Norway rat)

C:Date: 13-Jan-1996 #sequence_revision 01-Mar-1996 #text_change 20-Aug-1999
 C:Accession: S57953
 R:Hillard, A.; Thern, A.; Dahlback, B.
 submitted to the EMBL Data Library, July 1995
 A:Description: Molecular cloning of rat C4b-binding protein alpha- and beta-chains: s
 A:Reference number: S57953
 A:Accession: S57953
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-558 <HLI>
 A:Cross-references: EMBL:Z50051; NID:9899379; PIDN:CA930391.1; PID:9899380
 C:Superfamily: C4b-binding protein alpha chain; complement factor H repeat homology
 F:15-72/Domain: complement factor H repeat homology <FH1>
 F:77-134/Domain: complement factor H repeat homology <FH2>
 F:139-199/Domain: complement factor H repeat homology <FH3>
 F:204-258/Domain: complement factor H repeat homology <FH4>
 F:263-324/Domain: complement factor H repeat homology <FH5>
 F:328-386/Domain: complement factor H repeat homology <FH6>
 F:390-443/Domain: complement factor H repeat homology <FH7>
 F:447-501/Domain: complement factor H repeat homology <FH8>

Query Match 2.1%; Score 8; DB 2; Length 558;
 Best Local Similarity 100.0%; Pred. No. 18;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 213 WSDPLPEC 220
 |||||
 Db 127 WSDPLPEC 134

RESULT 13
 A37896
 progesterone receptor - chicken (fragments)
 C:Species: Gallus gallus (chicken)
 C:Date: 31-Jul-1991 #sequence_revision 31-Jul-1991 #text_change 31-Oct-1997
 C:Accession: A37896
 R:Denner, L.A.; Schrader, W.T.; O'Malley, B.W.; Welgell, N.L.
 J. Biol. Chem. 265, 16548-16555, 1990
 A:Title: Hormonal regulation and identification of chicken progesterone receptor phos
 A:Reference number: A37896; MUID:90375528; PMID:2398063
 A:Accession: A37896
 A:Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-42 <DEN>
 C:Superfamily: progesterone receptor; erba transforming protein homology
 C:Keywords: steroid hormone receptor; zinc finger

Query Match 1.8%; Score 7; DB 2; Length 42;
 Best Local Similarity 100.0%; Pred. No. 19;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PVPAPAL 12
 |||||
 Db 29 PVPAPAL 35

RESULT 14
 AE2201
 hypothetical protein asj164 [imported] - Nostoc sp. (strain PCC 7120)
 C:Species: Nostoc sp.
 A:Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
 C:Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 30-Jun-2002
 C:Accession: AE2201
 R:Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Irigu
 Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata
 DNA Res. 8, 205-213, 2001
 A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium
 A:Reference number: AB1807; MUID:21595285; PMID:11759840
 A:Accession: AE2201
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-98 <KUR>
 A:Cross-references: GB:BA000019; PIDN:BA874863.1; PID:917132259; GSPDB:GN00179

A:Experimental source: strain FCC 7120
 C:Genetics:
 A:Gene: as13164

Query Match 1.8%; Score 7; DB 2; Length 98;
 Best Local Similarity 100.0%; Pred. No. 39;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 21 LLLLVLL 27
 |||||
 Db 29 LLLLVLL 35

RESULT 15

AD0408
 conserved hypothetical protein YP03362 [Imported] - Yersinia pestis (strain CO92)

C:Species: Yersinia pestis
 C>Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Nov-2001
 C:Accession: AD0408
 R:Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.;
 deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.;
 11, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell, H.
 Nature 413, 523-527, 2001
 A:Title: Genome sequence of Yersinia pestis, the causative agent of plague.
 A:Reference number: AB0001; MUID:21470413; PMID:11586360

A:Accession: AD0408
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-106 <KUR>
 A:Cross-references: GB:AL590842; PIDN:CAC92592.1; PID:g15981289; GSPDB:GN00175
 C:Genetics:
 A:Gene: YP03362
 C:Superfamily: hypothetical protein HI0673

Query Match 1.8%; Score 7; DB 2; Length 106;
 Best Local Similarity 100.0%; Pred. No. 42;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 21 LLLLVLL 27
 |||||
 Db 6 LLLLVLL 12

Search completed: February 12, 2003, 11:11:57
 Job time : 25 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: February 12, 2003, 11:10:31 : Search time 13 Seconds
(without alignments)
748.779 Million cell updates/sec

Title: US-09-623-035-2

Perfect score: 381

Sequence: 1 MVARPSVPAALPLGLR.....HTCFTLLGLTIVTGLLT 381

Scoring table: OLIGO

Searched: 140259 seqs, 25548876 residues

Word size: 0

Total number of hits satisfying chosen parameters: 140259

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database: Published_Applications_AA:*

1: /cgn2_6/ptodata/1/pubppaa/US08_NEW_PUB.pep:*
2: /cgn2_6/ptodata/1/pubppaa/PCT_NEW_PUB.pep:*
3: /cgn2_6/ptodata/1/pubppaa/US06_NEW_PUB.pep:*
4: /cgn2_6/ptodata/1/pubppaa/US06_PUBCOMB.pep:*
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8: /cgn2_6/ptodata/1/pubppaa/US08_PUBCOMB.pep:*
9: /cgn2_6/ptodata/1/pubppaa/US09_NEW_PUB.pep:*
10: /cgn2_6/ptodata/1/pubppaa/US09_PUBCOMB.pep:*
11: /cgn2_6/ptodata/1/pubppaa/US10_NEW_PUB.pep:*
12: /cgn2_6/ptodata/1/pubppaa/US10_PUBCOMB.pep:*
13: /cgn2_6/ptodata/1/pubppaa/US60_NEW_PUB.pep:*
14: /cgn2_6/ptodata/1/pubppaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	65	17.1	182	10 US-09-925-299-1141	Sequence 1141, Ap
2	37	9.7	37	8 US-08-873-601-12	Sequence 12, Appl
3	37	9.7	37	9 US-09-792-630-65	Sequence 65, Appl
4	37	9.7	37	9 US-10-080-376-65	Sequence 65, Appl
5	37	9.7	37	9 US-10-061-395-13	Sequence 13, Appl
6	37	9.7	37	9 US-10-096-339-12	Sequence 12, Appl
7	37	9.7	37	10 US-09-157-748-19	Sequence 19, Appl
8	37	9.7	37	10 US-09-166-940-16	Sequence 16, Appl
9	37	9.7	37	10 US-09-922-503-9	Sequence 9, Appl
10	37	9.7	248	9 US-09-925-664-27	Sequence 27, Appl
11	37	9.7	261	9 US-09-925-664-30	Sequence 30, Appl
12	23	6.0	41	10 US-09-729-835-125	Sequence 125, Appl
13	10	2.6	263	10 US-09-800-729-88	Sequence 88, Appl
14	10	2.6	372	10 US-09-800-729-213	Sequence 213, Appl
15	9	2.4	345	9 US-09-924-340-106	Sequence 106, Appl
16	9	2.4	345	9 US-09-992-600A-106	Sequence 106, Appl
17	8	2.1	503	10 US-09-903-068-10	Sequence 10, Appl
18	7	1.8	34	10 US-09-864-761-43063	Sequence 43063, A
19	7	1.8	71	10 US-09-864-761-47821	Sequence 47821, A

20	7	1.8	86	10 US-09-764-860-544	Sequence 544, App
21	7	1.8	140	10 US-09-864-761-42549	Sequence 42549, A
22	7	1.8	155	10 US-09-925-297-504	Sequence 504, App
23	7	1.8	184	10 US-09-729-674-32	Sequence 32, Appl
24	7	1.8	184	10 US-09-925-297-737	Sequence 737, App
25	7	1.8	209	10 US-09-893-737-126	Sequence 126, App
26	7	1.8	224	9 US-09-975-719-175	Sequence 175, Appl
27	7	1.8	226	9 US-09-859-211-35	Sequence 35, Appl
28	7	1.8	230	9 US-10-063-547-60	Sequence 60, Appl
29	7	1.8	230	9 US-10-028-072-492	Sequence 492, App
30	7	1.8	230	9 US-10-063-616-80	Sequence 80, Appl
31	7	1.8	230	9 US-10-063-502-80	Sequence 80, Appl
32	7	1.8	230	9 US-10-121-049-492	Sequence 492, App
33	7	1.8	230	9 US-10-123-904-492	Sequence 492, App
34	7	1.8	230	9 US-10-140-470-492	Sequence 492, App
35	7	1.8	230	9 US-10-175-746-492	Sequence 492, App
36	7	1.8	230	9 US-10-176-918-492	Sequence 492, App
37	7	1.8	230	9 US-10-176-921-492	Sequence 492, App
38	7	1.8	230	10 US-09-949-192-35	Sequence 35, Appl
39	7	1.8	230	10 US-09-998-598-2590	Sequence 2590, App
40	7	1.8	230	10 US-10-006-867-80	Sequence 80, Appl
41	7	1.8	261	10 US-09-925-297-532	Sequence 532, App
42	7	1.8	276	9 US-09-895-913A-356	Sequence 356, App
43	7	1.8	297	10 US-09-925-302-609	Sequence 609, App
44	7	1.8	345	10 US-09-401-636-10	Sequence 10, Appl
45	7	1.8	347	10 US-09-886-055-155	Sequence 155, App

ALIGNMENTS

RESULT 1
US-09-925-299-1141
Sequence 1141, Application US/09925299
Patent No. US20020055627A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REFERENCE: PA102
CURRENT APPLICATION NUMBER: US/09/925,299
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05883
PRIOR FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: 60/124,270
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 1556
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1141
LENGTH: 182
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SITE
LOCATION: (123)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
LOCATION: (126)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
LOCATION: (129)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
LOCATION: (137)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
LOCATION: (143)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
LOCATION: (157)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
LOCATION: (165)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids

NAME/KEY: SITE
LOCATION: (165)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
LOCATION: (176)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-925-299-1141

Query Match 17.1%; Score 65; DB 10; Length 182;
Best Local Similarity 100.0%; Pred. No. 5.3e-50;
Matches 65; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 262 EHSIYCVNDEGEMSGPPGPECKRSKLSKYPYVOKPTVNVPTTEVSPTSOXTTKT 321
DB 3 EHSIYCVNDEGEMSGPPGPECKRSKLSKYPYVOKPTVNVPTTEVSPTSOXTTKT 62

QY 322 TPNAQ 326
DB 63 TPNAQ 67

RESULT 2
US-08-873-601-12
Sequence 12, Application US/08873601
Patent No. US20020064798A1
GENERAL INFORMATION:

APPLICANT: No. US20020064798A1an, Garry P.
TITLE OF INVENTION: COMBINATORIAL ENZYMATIC COMPLEXES
FILE REFERENCE: A-63915/DJB/RMS
CURRENT APPLICATION NUMBER: US/08/873,601
CURRENT FILING DATE: 1997-06-12
NUMBER OF SEQ ID NOS: 35
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 12
LENGTH: 37
TYPE: PRT
ORGANISM: Unknown
FEATURE:

OTHER INFORMATION: Description of Unknown Organism: UNKNOWN
US-08-873-601-12

Query Match 9.7%; Score 37; DB 8; Length 37;
Best Local Similarity 100.0%; Pred. No. 6.5e-26;
Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 345 PNKSGTSGTTRLLSGHTCFTLGLGLTVTMGLLT 381
DB 1 PNKSGTSGTTRLLSGHTCFTLGLGLTVTMGLLT 37

RESULT 3
US-09-792-630-65
Sequence 65, Application US/09792630
Patent No. US20020168640A1
GENERAL INFORMATION:
APPLICANT: Li, Min
TITLE OF INVENTION: BIOCHIPS COMPRISING NUCLEIC ACID/PROTEIN CONJUGATES
FILE REFERENCE: A-70295/RFT/RMS/RMK
CURRENT APPLICATION NUMBER: US/09/792,630
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 87
SOFTWARE: Patentin version 3.1
SEQ ID NO 65
LENGTH: 37
TYPE: PRT
ORGANISM: Rattus sp.
US-09-792-630-65

Query Match 9.7%; Score 37; DB 9; Length 37;
Best Local Similarity 100.0%; Pred. No. 6.5e-26;
Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 345 PNKSGTSGTTRLLSGHTCFTLGLGLTVTMGLLT 381
DB 1 PNKSGTSGTTRLLSGHTCFTLGLGLTVTMGLLT 37

RESULT 4
US-10-080-376-65
Sequence 65, Application US/10080376
Patent No. US20020172968A1
GENERAL INFORMATION:
APPLICANT: Li, Min
TITLE OF INVENTION: BIOCHIPS COMPRISING NUCLEIC ACID/PROTEIN CONJUGATES
FILE REFERENCE: A-70295-2/RFT/RMS/RMK
CURRENT APPLICATION NUMBER: US/10/080,376
CURRENT FILING DATE: 2000-02-19
PRIOR APPLICATION NUMBER: US 09/792,630
NUMBER OF SEQ ID NOS: 87
SOFTWARE: Patentin version 3.1
SEQ ID NO 65
LENGTH: 37
TYPE: PRT
ORGANISM: Rattus sp.
US-10-080-376-65

Query Match 9.7%; Score 37; DB 9; Length 37;
Best Local Similarity 100.0%; Pred. No. 6.5e-26;
Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 345 PNKSGTSGTTRLLSGHTCFTLGLGLTVTMGLLT 381
DB 1 PNKSGTSGTTRLLSGHTCFTLGLGLTVTMGLLT 37

RESULT 5
US-10-061-395-13
Sequence 13, Application US/10061395
Publication No. US20020192675A1
GENERAL INFORMATION:
APPLICANT: Zauderer, Maurice
TITLE OF INVENTION: Methods of Identifying Regulator Molecules
FILE REFERENCE: 1821.0080003
CURRENT APPLICATION NUMBER: US/10/061,395
CURRENT FILING DATE: 2002-02-04
PRIOR APPLICATION NUMBER: 60/271,423
PRIOR FILING DATE: 2001-02-27
PRIOR APPLICATION NUMBER: 60/265,880
PRIOR FILING DATE: 2001-02-05
PRIOR APPLICATION NUMBER: 60/265,589
PRIOR FILING DATE: 2001-02-02
NUMBER OF SEQ ID NOS: 116
SOFTWARE: Patentin version 3.1
SEQ ID NO 13
LENGTH: 37
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: DAF GPI anchor
US-10-061-395-13

Query Match 9.7%; Score 37; DB 9; Length 37;
Best Local Similarity 100.0%; Pred. No. 6.5e-26;
Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 345 PNKSGTSGTTRLLSGHTCFTLGLGLTVTMGLLT 381
DB 1 PNKSGTSGTTRLLSGHTCFTLGLGLTVTMGLLT 37

RESULT 6

US-10-096-339-12
; Sequence 12, Application US/10096339
; Publication No. US20030022196A1
; GENERAL INFORMATION:
; APPLICANT: Lorens, James B.
; APPLICANT: Kinsella, Todd
; APPLICANT: Masuda, Esteban
; APPLICANT: Hitoshi, Yasumichi
; APPLICANT: Liao, X. Charlene
; APPLICANT: Pearisall, Denise
; APPLICANT: Freira, Annabelle
; APPLICANT: Chu, Peter
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SCREENING FOR ALTERED CELLULAR PHENO
; FILE REFERENCE: A-71158/RMS/DCF
; CURRENT APPLICATION NUMBER: US/10/096,339
; CURRENT FILING DATE: 2002-03-08
; PRIOR APPLICATION NUMBER: US 09/076,624
; PRIOR FILING DATE: 1998-05-12
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 12
; LENGTH: 37
; TYPE: PRT
; ORGANISM: Rattus sp.
US-10-096-339-12

Query Match 9.7%; Score 37; DB 9; Length 37;
Best Local Similarity 100.0%; Pred. No. 6.5e-26;
Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 345 PNKSGTSGTTRLLSGHCTFLTGGLGLTVTMGLLT 381
DB 1 PNKSGTSGTTRLLSGHCTFLTGGLGLTVTMGLLT 37

RESULT 7
US-09-157-748-19
; Sequence 19, Application US/09157748
; Patent No. US20010003042A1
; GENERAL INFORMATION:
; APPLICANT: Lorens, James
; TITLE OF INVENTION: MULTIPARAMETER FACS ASSAYS TO DETECT ALTERATIONS IN
; FILE REFERENCE: A66587/DJB/RMS
; CURRENT APPLICATION NUMBER: US/09/157,748
; CURRENT FILING DATE: 1998-09-21
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 19
; LENGTH: 37
; TYPE: PRT
; ORGANISM: Homo sapiens
; PUBLICATION INFORMATION:
; JOURNAL: Nature
; VOLUME: 333
; ISSUE: 6170
; PAGES: 269-272
; DATE: 1988
; PUBLICATION INFORMATION:
; JOURNAL: J. Biol. Chem.
; VOLUME: 266
; PAGES: 1250-
; DATE: 1991
US-09-157-748-19

Query Match 9.7%; Score 37; DB 10; Length 37;
Best Local Similarity 100.0%; Pred. No. 6.5e-26;
Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 345 PNKSGTSGTTRLLSGHCTFLTGGLGLTVTMGLLT 381
DB 1 PNKSGTSGTTRLLSGHCTFLTGGLGLTVTMGLLT 37

RESULT 8
US-09-916-940-16
; Sequence 16, Application US/09916940
; Patent No. US20020127564A1
; GENERAL INFORMATION:
; APPLICANT: NO. US20020127564Alan, Garry P
; TITLE OF INVENTION: METHODS FOR SCREENING FOR TRANSDOMINANT INTRACELLULAR
; FILE REFERENCE: A-64260-6/RMS/AMS
; CURRENT APPLICATION NUMBER: US/09/916,940
; CURRENT FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: US 09/727,715
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US 08/963,368
; PRIOR FILING DATE: 1997-11-03
; PRIOR APPLICATION NUMBER: US 08/589,109
; PRIOR FILING DATE: 1996-01-23
; PRIOR APPLICATION NUMBER: US 08/589,911
; PRIOR FILING DATE: 1996-01-23
; PRIOR APPLICATION NUMBER: US 08/789,333
; PRIOR FILING DATE: 1997-01-23
; PRIOR APPLICATION NUMBER: US 08/787,738
; PRIOR FILING DATE: 1997-01-23
; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 16
; LENGTH: 37
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: membrane
US-09-916-940-16

Query Match 9.7%; Score 37; DB 10; Length 37;
Best Local Similarity 100.0%; Pred. No. 6.5e-26;
Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 345 PNKSGTSGTTRLLSGHCTFLTGGLGLTVTMGLLT 381
DB 1 PNKSGTSGTTRLLSGHCTFLTGGLGLTVTMGLLT 37

RESULT 9
US-09-922-503-9
; Sequence 9, Application US/09922503
; Patent No. US20020137022A1
; GENERAL INFORMATION:
; APPLICANT: Li, Min
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE CONSTRUCTION AND USE OF ENVEL
; FILE REFERENCE: A-69633-1/RT/RMS/RMK
; CURRENT APPLICATION NUMBER: US/09/922,503
; CURRENT FILING DATE: 2001-08-02
; PRIOR APPLICATION NUMBER: US 60/222,697
; PRIOR FILING DATE: 2000-08-02
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
; LENGTH: 37
; TYPE: PRT
; ORGANISM: Rattus sp.
US-09-922-503-9

Query Match 9.7%; Score 37; DB 10; Length 37;
Best Local Similarity 100.0%; Pred. No. 6.5e-26;
Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 345 PNKSGTSGTTRLLSGHCTFLTGGLGLTVTMGLLT 381
DB 1 PNKSGTSGTTRLLSGHCTFLTGGLGLTVTMGLLT 37

Db 118 VVEYECRPGY 127

RESULT 14
US-09-800-729-213

; Sequence 213, Application US/09800729
; Patent No. US20020068319A1
; GENERAL INFORMATION:
; APPLICANT: NI et al.
; TITLE OF INVENTION: 32 Human secreted proteins
; FILE REFERENCE: P2044P1
; CURRENT APPLICATION NUMBER: US/09/800/729
; CURRENT FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: PCT/US00/26013
; PRIOR FILING DATE: 2000-09-22
; PRIOR APPLICATION NUMBER: 60/155,709
; PRIOR FILING DATE: 1999-09-24
; NUMBER OF SEQ ID NOS: 217
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 213
; LENGTH: 372
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-800-729-213

Query Match

Best Local Similarity 100.0%; Score 10; DB 10; Length 372;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 124 VVEYECRPGY 133

Db 118 VVEYECRPGY 127

RESULT 15
US-09-924-340-106

; Sequence 106, Application US/09924340
; Publication No. US20030027248A1
; GENERAL INFORMATION:
; APPLICANT: Bejanin, Stephanie
; APPLICANT: Tanaka, Hiroaki
; TITLE OF INVENTION: HUMAN CDMS AND PROTEINS AND USES THEREOF
; FILE REFERENCE: 91.US2.REG
; CURRENT APPLICATION NUMBER: US/09/924,340
; CURRENT FILING DATE: 2001-08-06
; PRIOR APPLICATION NUMBER: US 60/305,456
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/302,277
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 60/298,698
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: US 60/293,574
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: JPatent
; SEQ ID NO 106
; LENGTH: 345
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: 1..19
US-09-924-340-106

Query Match

Best Local Similarity 100.0%; Score 9; DB 9; Length 345;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 185 TISFSCNTG 193

Db 105 TISFSCNTG 113

Search completed: February 12, 2003, 11:12:38
Job time : 14 secs

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OM protein - protein search, using sw model

Run on: February 12, 2003, 11:09:46 ; Search time 16 Seconds
(without alignments)
700.633 Million cell updates/sec

Title: US-09-623-035-2

Perfect score: 381
Sequence: 1 MTVPAPVPAALPLGLGELPR.....HTCPTLTGLGLTVWGLLT 381

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Gapop 60.0 , Gapext 60.0

Searched: 262574 seqs, 29422922 residues

Word size : 0

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

Issued_Patents_AA:*
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2: /cgn2_6/prodata/1/1aa/5B.COMB.pep:*
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6: /cgn2_6/prodata/1/1aa/Backfilest1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	323	84.8	323	2	US-08-435-149-2
2	323	84.8	577	2	US-08-435-149-3
3	323	84.8	611	4	US-09-475-460A-32
4	323	84.8	611	4	US-09-748-061A-32
5	273	71.7	324	1	US-08-310-416A-14
6	273	71.7	324	2	US-08-888-171-14
7	128	33.6	128	6	5514582-42
8	37	9.7	37	4	US-08-789-333E-16
9	37	9.7	37	4	US-09-133-944-16
10	37	9.7	37	4	US-09-208-827-17
11	37	9.7	37	4	US-08-787-738B-16
12	37	9.7	37	4	US-09-157-748-19
13	37	9.7	42	1	US-08-004-492-4
14	37	9.7	42	1	US-08-004-492-7
15	37	9.7	102	1	US-08-282-951-2
16	37	9.7	248	1	US-08-644-664B-27
17	37	9.7	248	2	US-08-761-277A-27
18	37	9.7	261	1	US-08-644-664B-30
19	37	9.7	261	2	US-08-761-277A-30
20	37	9.7	272	1	US-08-282-951-6
21	29	7.6	36	4	US-09-169-015-26
22	23	6.0	41	4	US-09-257-179-125
23	22	5.8	23	1	US-07-811-048-8
24	9	2.4	128	6	5514582-34
25	9	2.4	181	2	US-08-640-977-3
26	9	2.4	248	2	US-08-640-977-2
27	9	2.4	266	2	US-08-640-977-4

28	9	2.4	326	2	US-08-640-977-1	Sequence 1, Appl1
29	8	2.1	8	1	US-08-210-266A-4	Sequence 4, Appl1
30	8	2.1	8	1	US-08-688-675-4	Sequence 4, Appl1
31	8	2.1	8	3	US-08-477-860C-4	Sequence 2, Appl1
32	8	2.1	363	4	US-08-681-234B-2	Sequence 10, Appl1
33	8	2.1	503	4	US-09-382-256-10	Sequence 10, Appl1
34	8	2.1	503	4	US-09-395-115-10	Sequence 10, Appl1
35	8	2.1	503	4	US-08-436-265-10	Sequence 10, Appl1
36	8	2.1	503	4	US-09-679-187-10	Sequence 10, Appl1
37	7	1.8	7	1	US-08-210-266A-5	Sequence 5, Appl1
38	7	1.8	7	1	US-08-688-675-5	Sequence 5, Appl1
39	7	1.8	7	3	US-08-477-860C-5	Sequence 5, Appl1
40	7	1.8	23	2	US-08-652-450A-16	Sequence 16, Appl1
41	7	1.8	60	1	US-08-210-266A-10	Sequence 10, Appl1
42	7	1.8	60	1	US-08-688-675-10	Sequence 10, Appl1
43	7	1.8	60	3	US-08-477-860C-10	Sequence 10, Appl1
44	7	1.8	89	4	US-09-134-001C-4553	Sequence 14, Appl1
45	7	1.8	109	4	US-09-071-035-194	Sequence 194, Appl1

ALIGNMENTS

RESULT 1
US-08-435-149-2
; Sequence 2, Application US/08435149
; Patent No. 5866402
GENERAL INFORMATION:
; APPLICANT: INNIS, MICHAEL A.
; APPLICANT: ZAROR, ISABEL
; APPLICANT: CREASEY, ABIA A.
; TITLE OF INVENTION: CHIMERIC MCP AND DAF PROTEINS WITH CELL
; TITLE OF INVENTION: SURFACE LOCALIZING DOMAIN
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CHIRON CORPORATION
; STREET: INTELLECTUAL PROPERTY - R440, P.O. BOX 8097
; CITY: EMERYVILLE
; STATE: CALIFORNIA
; COUNTRY: U.S.A.
; ZIP: 94662-8097
COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/435,149
; FILING DATE: 05-MAY-1995
; CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
; NAME: SAVERIDE, PAUL B.
; REGISTRATION NUMBER: 36,914
; REFERENCE/DOCKET NUMBER: 0989,001
TELECOMMUNICATION INFORMATION:
; TELEPHONE: (510) 601-2585
; TELEFAX: (510) 655-3542
; TELETYPE: N/A
; INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
; LENGTH: 323 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-435-149-2
Query Match 84.8%; Score 323; DB 2; Length 323;
Best Local Similarity 100.0%; Pred No. 1.8e-306;
Matches 323; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
35 DCGIPDPVPAAPALBGRSTFPEDTVTYKCESEFVRIPEKDKSVICLKSGNSDIEFC 94
|||||

5264357

Db 1 DCGLPDVPNAPALEGRISFPEDEVITYIKCEESFYKILGKEDSVYCLKGSQMSDIEERC 60
QY 95 NNSCEVPTRLNLSASLKOPYITTONYFPGTVVEYECRPGYRRRPSLSPKLTCLONLKMSWA 154
Db 61 NNSCEVPTRLNLSASLKOPYITTONYFPGTVVEYECRPGYRRRPSLSPKLTCLONLKMSWA 120
QY 155 VEFCKKSCPNNGEIRNGOIVPGGILFGATISFSCNTGYKILFGSTSSFCILSGSSVOMS 214
Db 121 VEFCKKSCPNNGEIRNGOIVPGGILFGATISFSCNTGYKILFGSTSSFCILSGSSVOMS 180
QY 215 DPLPCEREIYCAPPOINDGIIQGERDHYGYROSYYACNKGFTMIGESITCTVNNDEG 274
Db 181 DPLPCEREIYCAPPOINDGIIQGERDHYGYROSYYACNKGFTMIGESITCTVNNDEG 240
QY 275 EMSGPPPECRGKSLTSKVPPTVQKPTTVVPTTEVSPTSQKTTTTPPNAQATSTPVS 334
Db 241 EMSGPPPECRGKSLTSKVPPTVQKPTTVVPTTEVSPTSQKTTTTPPNAQATSTPVS 300
QY 335 RTTKHFHETTPNKGSGTTSGTTR 357
Db 301 RTTKHFHETTPNKGSGTTSGTTR 323

RESULT 2

US-08-435-149-3
; Sequence 3, Application US/08435149
; Patent No. 5866402
; GENERAL INFORMATION:
; APPLICANT: INNIS, MICHAEL A.
; APPLICANT: ZAROR, ISABEL
; TITLE OF INVENTION: CHIMERIC MCP AND DAF PROTEINS WITH CELL
; TITLE OF INVENTION: SURFACE LOCALIZING DOMAIN
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CHIRON CORPORATION
; STREET: INTELLECTUAL PROPERTY - R440, P.O. BOX 8097
; CITY: EMERYVILLE
; STATE: CALIFORNIA
; COUNTRY: U.S.A.
; ZIP: 94662-8097
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/435,149
; FILING DATE: 05-MAY-1995
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: SAVEREIDE, PAUL B.
; REGISTRATION NUMBER: 36,914
; REFERENCE/DOCKET NUMBER: 0989,001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (510) 601-2585
; TELEFAX: (510) 655-3542
; TELEX: N/A
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 577 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-435-149-3

Query Match 84.8%; Score 323; DB 2; Length 577;
Best Local Similarity 100.0%; Pred. No. 3,1e-306;
Matches 323; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 35 DCGLPDVPNAPALEGRISFPEDEVITYIKCEESFYKILGKEDSVYCLKGSQMSDIEERC 94
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Db 255 DCGLPDVPNAPALEGRISFPEDEVITYIKCEESFYKILGKEDSVYCLKGSQMSDIEERC 314
QY 95 NNSCEVPTRLNLSASLKOPYITTONYFPGTVVEYECRPGYRRRPSLSPKLTCLONLKMSWA 154
Db 315 NNSCEVPTRLNLSASLKOPYITTONYFPGTVVEYECRPGYRRRPSLSPKLTCLONLKMSWA 374
QY 155 VEFCKKSCPNNGEIRNGOIVPGGILFGATISFSCNTGYKILFGSTSSFCILSGSSVOMS 214
Db 375 VEFCKKSCPNNGEIRNGOIVPGGILFGATISFSCNTGYKILFGSTSSFCILSGSSVOMS 434
QY 215 DPLPCEREIYCAPPOINDGIIQGERDHYGYROSYYACNKGFTMIGESITCTVNNDEG 274
Db 435 DPLPCEREIYCAPPOINDGIIQGERDHYGYROSYYACNKGFTMIGESITCTVNNDEG 494
QY 275 EMSGPPPECRGKSLTSKVPPTVQKPTTVVPTTEVSPTSQKTTTTPPNAQATSTPVS 334
Db 495 EMSGPPPECRGKSLTSKVPPTVQKPTTVVPTTEVSPTSQKTTTTPPNAQATSTPVS 554
QY 335 RTTKHFHETTPNKGSGTTSGTTR 357
Db 555 RTTKHFHETTPNKGSGTTSGTTR 577

RESULT 3

US-09-475-460A-32
; Sequence 32, Application US/09475460A
; Patent No. 6316253
; GENERAL INFORMATION:
; APPLICANT: Scott, Elizabeth
; APPLICANT: Innis, Michael
; TITLE OF INVENTION: EXPRESSION VECTORS, TRANSFECTION SYSTEMS, AND METHOD OF
; TITLE OF INVENTION: USE THEREOF
; FILE REFERENCE: 1527,003
; CURRENT APPLICATION NUMBER: US/09/475,460A
; CURRENT FILING DATE: 1999-12-30
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 32
; LENGTH: 611
; TYPE: PRT
; ORGANISM: CAB2
US-09-475-460A-32

Query Match 84.8%; Score 323; DB 4; Length 611;
Best Local Similarity 100.0%; Pred. No. 3,2e-306;
Matches 323; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 35 DCGLPDVPNAPALEGRISFPEDEVITYIKCEESFYKILGKEDSVYCLKGSQMSDIEERC 94
Db 289 DCGLPDVPNAPALEGRISFPEDEVITYIKCEESFYKILGKEDSVYCLKGSQMSDIEERC 348
QY 95 NNSCEVPTRLNLSASLKOPYITTONYFPGTVVEYECRPGYRRRPSLSPKLTCLONLKMSWA 154
Db 349 NNSCEVPTRLNLSASLKOPYITTONYFPGTVVEYECRPGYRRRPSLSPKLTCLONLKMSWA 408
QY 155 VEFCKKSCPNNGEIRNGOIVPGGILFGATISFSCNTGYKILFGSTSSFCILSGSSVOMS 214
Db 409 VEFCKKSCPNNGEIRNGOIVPGGILFGATISFSCNTGYKILFGSTSSFCILSGSSVOMS 468
QY 215 DPLPCEREIYCAPPOINDGIIQGERDHYGYROSYYACNKGFTMIGESITCTVNNDEG 274
Db 469 DPLPCEREIYCAPPOINDGIIQGERDHYGYROSYYACNKGFTMIGESITCTVNNDEG 528
QY 275 EMSGPPPECRGKSLTSKVPPTVQKPTTVVPTTEVSPTSQKTTTTPPNAQATSTPVS 334
Db 529 EMSGPPPECRGKSLTSKVPPTVQKPTTVVPTTEVSPTSQKTTTTPPNAQATSTPVS 588
QY 335 RTTKHFHETTPNKGSGTTSGTTR 357
Db 589 RTTKHFHETTPNKGSGTTSGTTR 611

RESULT 4

US-09-748-061A-32
; Sequence 32, Application US/09748061A
; Patent No. 6451539
; GENERAL INFORMATION:
; APPLICANT: Scott, Elizabeth
; APPLICANT: Innis, Michael
; TITLE OF INVENTION: EXPRESSION VECTORS, TRANSFECTION SYSTEMS, AND METHOD OF
; FILE REFERENCE: PP01527.101 / 2302-1527.10
; CURRENT APPLICATION NUMBER: US/09/748,061A
; CURRENT FILING DATE: 2000-12-22
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 32
; LENGTH: 611
; TYPE: PR1
; ORGANISM: CAB2
US-09-748-061A-32

Query Match 84.8%; Score 323; DB 4; Length 611;
Best Local Similarity 100.0%; Pred. No. 3.2e-306;
Matches 323; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 35 DCGLPVPYNAQPALEGRTPEDVTITTKCESEFVKIPGEKDSVTLKGSQMSDIEEFC 94
DB 289 DCGLPVPYNAQPALEGRTPEDVTITTKCESEFVKIPGEKDSVTLKGSQMSDIEEFC 348
QY 95 NRSCEVPTLNSASLKQPYTONYEPYGVVYECRPGYRREPSISPLTCTLOMLKMTA 154
DB 349 NRSEVPTLNSASLKQPYTONYEPYGVVYECRPGYRREPSISPLTCTLOMLKMTA 408
QY 155 VEFCKKSCPNPGEIRNGQIDVPGLFGATISFCNTGYKLFGSTSFCLISGSVQMS 214
DB 409 VEFCKKSCPNPGEIRNGQIDVPGLFGATISFCNTGYKLFGSTSFCLISGSVQMS 468
QY 215 DPLECEETIYCPAPQIDNGIIGERDHYGRQSVYACNKGFTMIGHSITCVNNDG 274
DB 469 DPLECEETIYCPAPQIDNGIIGERDHYGRQSVYACNKGFTMIGHSITCVNNDG 528
QY 275 EMSGPPPCRGKSLTSKVPYVOKPTVNVPTTEVSPTOKTTTKTTPNAQATRSPPVS 334
DB 529 EMSGPPPCRGKSLTSKVPYVOKPTVNVPTTEVSPTOKTTTKTTPNAQATRSPPVS 588
QY 335 RTTKHFHTTPNKGSGTTSCTTR 357
DB 589 RTTKHFHTTPNKGSGTTSCTTR 611

RESULT 5
US-08-310-416A-14
; Sequence 14, Application US/08310416A
; Patent No. 5679546
; GENERAL INFORMATION:
; APPLICANT: Jone-Long Ko et al.
; TITLE OF INVENTION: CHIMERIC PROTEINS WHICH BLOCK
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 MB
; COMPUTER: IBM PS/2 Model 50Z or 55SX
; OPERATING SYSTEM: MS-DOS (Version 5.0)
; SOFTWARE: WordPerfect (Version 5.1)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/310,416A
; FILING DATE: 22-SEP-1994
; CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:
; NAME: Paul T. Clark
; REGISTRATION NUMBER: 30,162
; REFERENCE/DOCKET NUMBER: 06180/005001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-5070
; TELEFAX: (617) 542-8906
; TELE: 200154
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 324 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-310-416A-14

Query Match 71.7%; Score 273; DB 1; Length 324;
Best Local Similarity 100.0%; Pred. No. 8.7e-258;
Matches 273; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 86 QMSDIEEFCNRSCEVPTLNSASLKQPYTONYEPYGVVYECRPGYRREPSISPKLTC 145
DB 52 QMSDIEEFCNRSCEVPTLNSASLKQPYTONYEPYGVVYECRPGYRREPSISPKLTC 111
QY 146 LONLKMSTAVFECKKSCPNPGEIRNGQIDVPGLFGATISFCNTGYKLFGSTSFCL 205
DB 112 LONLKMSTAVFECKKSCPNPGEIRNGQIDVPGLFGATISFCNTGYKLFGSTSFCL 171
QY 206 ISSGVQMSDPLPECEETIYCPAPQIDNGIIGERDHYGRQSVYACNKGFTMIGHSI 265
DB 172 ISSGVQMSDPLPECEETIYCPAPQIDNGIIGERDHYGRQSVYACNKGFTMIGHSI 231
QY 266 YCTVNNDEGMSGPPPCRGKSLTSKVPYVOKPTVNVPTTEVSPTOKTTTKTTPNA 325
DB 232 YCTVNNDEGMSGPPPCRGKSLTSKVPYVOKPTVNVPTTEVSPTOKTTTKTTPNA 291
QY 326 QATRSPTVSRRTTKHFHTTPNKGSGTTSCTTR 358
DB 292 QATRSPTVSRRTTKHFHTTPNKGSGTTSCTTR 324

RESULT 6
US-08-888-171-14
; Sequence 14, Application US/08888171
; Patent No. 5851528
; GENERAL INFORMATION:
; APPLICANT: Jone-Long, Ko
; APPLICANT: Higgins, Paul J.
; APPLICANT: Yeh, C. Grace
; TITLE OF INVENTION: METHODS OF INHIBITING COMPLEMENT
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/888,171
; FILING DATE: 03-JUL-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/310,416
; FILING DATE: 22-SEP-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Freeman, John W.

REGISTRATION NUMBER: 29,066
REFERENCE/DOCKET NUMBER: 06180/005002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-507
TELEFAX: 617/542-890
TELEX: 200154
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 324 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-888-171-14

Query Match 71.7%: Score 273; DB 2; Length 324;
Best Local Similarity 100.0%: Pred. No. 8.7e-258;
Matches 273; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 86 QMSDIEFCNRSCVEPTRLNSASIKOPYITQNTFPGVVEYECRPGYRREPSLPKLTG 145
DB 52 QMSDIEFCNRSCVEPTRLNSASIKOPYITQNTFPGVVEYECRPGYRREPSLPKLTG 111
QY 146 LQMLKSTAVEFCCKKSCPNPGEIRNGQIDVPGGILFGATISFSCNTGYKLFGSTSFCL 205
DB 112 LQMLKSTAVEFCCKKSCPNPGEIRNGQIDVPGGILFGATISFSCNTGYKLFGSTSFCL 171
QY 206 ISSSVQMSDPLPECRRTYCPAPPOIDNGIIOGERDHYGRQSTYACNKGFTMIGHST 265
DB 172 ISSSVQMSDPLPECRRTYCPAPPOIDNGIIOGERDHYGRQSTYACNKGFTMIGHST 231
QY 266 YCTVNNDEGEMSGPPECRCRSLTSKVPPTVQKPTTVNVPTEVSPTOKTKTTTPNA 325
DB 232 YCTVNNDEGEMSGPPECRCRSLTSKVPPTVQKPTTVNVPTEVSPTOKTKTTTPNA 291
QY 326 QATRSIPVSTTTHFHETTPNKGSGTTSGTTRL 358
DB 292 QATRSIPVSTTTHFHETTPNKGSGTTSGTTRL 324

RESULT 7
5514582-42
Patent No. 5514582
APPLICANT: CAPON, DANIEL J.; LASKY, LAURENCE A.
TITLE OF INVENTION: RECOMBINANT DNA ENCODING HYBRID
IMMUNOGLOBULINS
NUMBER OF SEQUENCES: 43
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/185,670
FILING DATE: 21-JAN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 986,931
FILING DATE: 08-DEC-1992
APPLICATION NUMBER: 808,122
FILING DATE: 16-DEC-1991
APPLICATION NUMBER: 440,625
FILING DATE: 22-NOV-1989
APPLICATION NUMBER: 315,015
FILING DATE: 23-FEB-1989
SEQ ID NO: 42
LENGTH: 128
5514582-42

Query Match 33.6%: Score 128; DB 6; Length 128;
Best Local Similarity 100.0%: Pred. No. 5.6e-117;
Matches 128; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 99 EYPTRLNSASIKOPYITQNTFPGVVEYECRPGYRREPSLPKLTCLQNLKSTAVEFC 158
DB 1 EYPTRLNSASIKOPYITQNTFPGVVEYECRPGYRREPSLPKLTCLQNLKSTAVEFC 60
QY 159 KKKSCPNPGEIRNGQIDVPGGILFGATISFSCNTGYKLFGSTSFCLISSSVQMSDPLP 218
DB 61 KKKSCPNPGEIRNGQIDVPGGILFGATISFSCNTGYKLFGSTSFCLISSSVQMSDPLP 120

QY 219 ECREIYCP 226
DB 121 ECREIYCP 128

RESULT 8
US-08-789-333F-16
Sequence 16, Application US/08/789333F
Patent No. 6153380
GENERAL INFORMATION:
APPLICANT: No. 6153380an, Garry P
APPLICANT: Rothenberg, S. M.
TITLE OF INVENTION: METHODS FOR SCREENING FOR TRANSDOMINANT INTRACELLULAR
FILE REFERENCE: A642601DJBMSDS
CURRENT APPLICATION NUMBER: US/08/789,333F
CURRENT FILING DATE: 1997-01-23
PRIOR FILING DATE: 1996-01-23
PRIOR APPLICATION NUMBER: 08/589,108
PRIOR FILING DATE: 1996-01-23
NUMBER OF SEQ ID NOS: 102
SOFTWARE: Patentln Ver. 2.0
SEQ ID NO 16
LENGTH: 37
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: membrane
US-08-789-333F-16

Query Match 9.7%: Score 37; DB 4; Length 37;
Best Local Similarity 100.0%: Pred. No. 7.2e-29;
Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 345 PNKSGTSGTTRLNSGHTCFTLTGLGLTVTMGLLT 381
DB 1 PNKSGTSGTTRLNSGHTCFTLTGLGLTVTMGLLT 37

RESULT 9
US-09-133-944-16
Sequence 16, Application US/09133944
Patent No. 6280937
GENERAL INFORMATION:
APPLICANT: Luo, Ying
APPLICANT: Yu, Pei Wen
APPLICANT: Lorens, James
TITLE OF INVENTION: SHUTTLE VECTORS
FILE REFERENCE: A66252/DJB/DAV
CURRENT APPLICATION NUMBER: US/09/133,944
CURRENT FILING DATE: 1999-08-14
EARLIER APPLICATION NUMBER: 09/133,949
EARLIER FILING DATE: 1998-08-14
NUMBER OF SEQ ID NOS: 39
SOFTWARE: Patentln Ver. 2.0
SEQ ID NO 16
LENGTH: 37
TYPE: PRT
ORGANISM: Unknown
FEATURE:
OTHER INFORMATION: Description of Unknown Organism: anchor site
PUBLICATION INFORMATION:
JOURNAL: Nature
VOLUME: 333
ISSUE: 6170
PAGES: 269-272
DATE: 1998
PUBLICATION INFORMATION:
JOURNAL: J. Biol. Chem.
VOLUME: 266

PAGES: 1250-1250
DATE: 1991
US-09-133-944-16

Query Match 9.7%: Score 37; DB 4; Length 37;
Best Local Similarity 100.0%; Pred. No. 7.2e-29;
Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 345 PNKSGTTSCTTRLSSGHTCTTGLGTLVTMGLT 381
DB 1 PNKSGTTSCTTRLSSGHTCTTGLGTLVTMGLT 37

RESULT 10

US-09-208-827-17
Sequence 17, Application US/09208827
Patent No. 6391582
GENERAL INFORMATION:
APPLICANT: Luo, Ying
APPLICANT: Yu, Pei Wen
APPLICANT: Lorens, James
TITLE OF INVENTION: SHUTTLE VECTORS
FILE REFERENCE: A66252-1/DB/DAV
CURRENT APPLICATION NUMBER: US/09/208,827
CURRENT FILING DATE: 1998-12-09
EARLIER APPLICATION NUMBER: 09/133,949
EARLIER FILING DATE: 1998-08-14
NUMBER OF SEQ ID NOS: 43
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 17
LENGTH: 37
TYPE: PRT
ORGANISM: Unknown
FEATURE:
OTHER INFORMATION: Description of Unknown Organism: anchor site
PUBLICATION INFORMATION:
JOURNAL: Nature
VOLUME: 333
ISSUE: 6170
PAGES: 269-272
DATE: 1988
PUBLICATION INFORMATION:
JOURNAL: J. Biol. Chem.
VOLUME: 266
PAGES: 1250-1250
DATE: 1991
US-09-208-827-17

Query Match 9.7%: Score 37; DB 4; Length 37;
Best Local Similarity 100.0%; Pred. No. 7.2e-29;
Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 345 PNKSGTTSCTTRLSSGHTCTTGLGTLVTMGLT 381
DB 1 PNKSGTTSCTTRLSSGHTCTTGLGTLVTMGLT 37

RESULT 11

US-08-787-738B-16
Sequence 16, Application US/08787738B
Patent No. 6455247
GENERAL INFORMATION:
APPLICANT: Rothenbury, Michael S.
TITLE OF INVENTION: METHODS FOR SCREENING FOR TRANSDOMINANT EFFECTOR
FILE REFERENCE: A-64259-1 correction
CURRENT APPLICATION NUMBER: US/08/787,738B
CURRENT FILING DATE: 2001-09-18
PRIOR APPLICATION NUMBER: 08/589,108
PRIOR FILING DATE: 1996-01-23
PRIOR APPLICATION NUMBER: 08/589,911
PRIOR FILING DATE: 1996-01-23

NUMBER OF SEQ ID NOS: 97
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 16
LENGTH: 37
TYPE: PRT
ORGANISM: Rattus sp.
US-08-787-738B-16

Query Match 9.7%: Score 37; DB 4; Length 37;
Best Local Similarity 100.0%; Pred. No. 7.2e-29;
Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 345 PNKSGTTSCTTRLSSGHTCTTGLGTLVTMGLT 381
DB 1 PNKSGTTSCTTRLSSGHTCTTGLGTLVTMGLT 37

RESULT 12

US-09-157-748-19
Sequence 19, Application US/09157748
Patent No. 6461813
GENERAL INFORMATION:
APPLICANT: Lorens, James
TITLE OF INVENTION: Multiparameter FACS Assays to Detect Alterations in
FILE REFERENCE: A66587/DB/RMS
CURRENT APPLICATION NUMBER: US/09/157,748
CURRENT FILING DATE: 1998-09-21
NUMBER OF SEQ ID NOS: 46
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 19
LENGTH: 37
TYPE: PRT
ORGANISM: Homo sapiens
PUBLICATION INFORMATION:
JOURNAL: Nature
VOLUME: 333
ISSUE: 6170
PAGES: 269-272
DATE: 1988
PUBLICATION INFORMATION:
JOURNAL: J. Biol. Chem.
VOLUME: 266
PAGES: 1250-
DATE: 1991
US-09-157-748-19

Query Match 9.7%: Score 37; DB 4; Length 37;
Best Local Similarity 100.0%; Pred. No. 7.2e-29;
Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 345 PNKSGTTSCTTRLSSGHTCTTGLGTLVTMGLT 381
DB 1 PNKSGTTSCTTRLSSGHTCTTGLGTLVTMGLT 37

RESULT 13

US-08-004-492-4
Sequence 4, Application US/08004492
Patent No. 5623053
GENERAL INFORMATION:
APPLICANT: Gastinel, Louis N.
APPLICANT: Bjorkman, Pamela J.
TITLE OF INVENTION: Soluble Mammal-Derived FC Receptor which Binds at a pH Rang
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESS: Shirley L. Church
STREET: 1063 Morse Avenue, #11-306
CITY: Sunnyvale
STATE: CA
COUNTRY: U.S.A.
ZIP: 94089
COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.5 inch, 1.44mb storage
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: EPO Patentin 1.30/Edited in Microsoft Word 7.0, saved in "text onl
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/004,492
FILING DATE: 14-JAN-1993
CLASSIFICATION: 435
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 07/819,413
FILING DATE: 10-JAN-1992
ATTORNEY/AGENT INFORMATION:
NAME: Church, Shirley L.
REGISTRATION NUMBER: 31,858
REFERENCE/DOCKET NUMBER: CIT2120
TELECOMMUNICATION INFORMATION:
TELEPHONE: (408) 745-1567
TELEFAX: (408) 747-1109
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 42 amino acid residues
TYPE: Amino acid
STRANDEDNESS:
TOPOLOGY: Linear
MOLECULE TYPE: Protein/Peptide
HYPOTHETICAL: NO
ANTI-SENSE:
FRAGMENT TYPE: C-terminal fragment
ORIGINAL SOURCE:
ORGANISM: FcRn from Rattus norvegicus DAF from Homo sapiens
STRAIN:
INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE: FcRn from 11 day old/germ-line
HAPLOTYPE:
TISSUE TYPE: FcRn from proximal third of small intestine
CELL TYPE: FcRn from epithelial cells
CELL LINE: DAF from Hela cells
ORGANELLE:
IMMEDIATE SOURCE:
LIBRARY:
CLONE: 'p-51-DAF' cell line produces chimeric FcRn heavy chain with
POSITION IN GENOME:
CHROMOSOME/SEGMENT:
MAP POSITION:
UNITS:
FEATURE:
NAME/KEY: The insertion of the DAF amino acid sequence after the Fc
LOCATION: FcRn heavy chain (a.a. 265 to 269) from 1 to 5, DAF (a.a.
IDENTIFICATION METHOD: The cell surface expression of lipid-linked
OTHER INFORMATION: Intracellular modification results in the removal
PUBLICATION INFORMATION:
AUTHORS: Gastinel, Louis N.
AUTHORS: Simister, N.E.
AUTHORS: Bjorkman, P.J.
TITLE: Expression and Crystallization of a Soluble and Functional
JOURNAL: Proc. Natl. Acad. Sci. U.S.A.
VOLUME: 89
ISSUE:
PAGES: 638-642
DATE:
DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO: 4: FROM 1 TO 42
US-08-004-492-4

Query Match 9.7%; Score 37; DB 1; Length 42;
Best Local Similarity 100.0%; Pred. No. 8.1e-29;
Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 345 PKNQSGTSGTTRLISGHTCFITLGLGLTVMGILLT 381
|||||

DB 6 PKNQSGTSGTTRLISGHTCFITLGLGLTVMGILLT 42

RESULT 14
US-08-004-492-7
Sequence 7, Application US/08004492
Patent No. 5623053
GENERAL INFORMATION:
APPLICANT: Gastinel, Louis N.
APPLICANT: Bjorkman, Pamela J.
TITLE OF INVENTION: Soluble Mammal-Derived Fc Receptor Which Binds at a pH Rang
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSER: Shirley L. Church
STREET: 1063 Morse Avenue, #11-306
CITY: Sunnyvale
STATE: CA
COUNTRY: U.S.A.
ZIP: 94089
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44mb storage
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: EPO Patentin 1.30/Edited in Microsoft Word 7.0, saved in "text onl
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/004,492
FILING DATE: 14-JAN-1993
CLASSIFICATION: 435
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 07/819,413
FILING DATE: 10-JAN-1992
ATTORNEY/AGENT INFORMATION:
NAME: Church, Shirley L.
REGISTRATION NUMBER: 31,858
REFERENCE/DOCKET NUMBER: CIT2120
TELECOMMUNICATION INFORMATION:
TELEPHONE: (408) 745-1567
TELEFAX: (408) 747-1109
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 42 amino acid residues
TYPE: Amino acid
STRANDEDNESS:
TOPOLOGY: Linear
MOLECULE TYPE: Protein/Peptide
HYPOTHETICAL: NO
ANTI-SENSE:
FRAGMENT TYPE: C-terminal
ORIGINAL SOURCE:
ORGANISM: Beta 2-M from Rattus norvegicus DAF from Homo sapiens
STRAIN: Beta 2-M from Sprague-Dawley
INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE:
HAPLOTYPE:
TISSUE TYPE:
CELL TYPE:
CELL LINE: DAF from Hela cells
ORGANELLE:
IMMEDIATE SOURCE:
LIBRARY:
CLONE: Beta 2m-DAF' cell line produces chimeric rat beta 2-microglo
POSITION IN GENOME:
CHROMOSOME/SEGMENT:
MAP POSITION:
UNITS:
FEATURE:
NAME/KEY: The insertion of the DAF amino acid sequence after the C-
LOCATION: Rat beta 2-microglobulin (a.a. 95 to 99) from 1 to 5 DAF
IDENTIFICATION METHOD: The cell surface expression of lipid-linked
OTHER INFORMATION: Intracellular modification results in the removal
PUBLICATION INFORMATION:
AUTHORS: Gastinel, Louis N.
AUTHORS: Simister, N.E.

Search completed: February 12, 2003, 11:12:18
Job time : 17 secs

AUTHORS: Bjorkman, P.J.
TITLE: Expression and Crystallization of a Soluble and Functional f
JOURNAL: Proc. Natl. Acad. Sci. U.S.A.
VOLUME: 89
ISSUE:
PAGES: 638-642
DATE:
DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE: 16-Jan-1992
RELEVANT RESIDUES IN SEQ ID NO: 7 : FROM 1 TO 42
US-08-004-492-7

Query Match 9.7%; Score 37; DB 1; Length 42;
Best Local Similarity 100.0%; Pred. No. 8.1e-29;
Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 345 PNKSGTSGTTRLISGHTCTLTGLTGLTVMGLLT 381
DB 6 PNKSGTSGTTRLISGHTCTLTGLTGLTVMGLLT 42

RESULT 15

US-08-282-951-2
Sequence 2, Application US/08282951
Patent No. 5665590
GENERAL INFORMATION:
APPLICANT: YANG, ZHI
TITLE OF INVENTION: METHOD FOR ISOLATING AND DIRECTLY
TITLE OF INVENTION: CLONING GENES WHICH ENCODE CELL-SURFACE AND SECRETED
TITLE OF INVENTION: PROTEINS
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morrlson & Foerster
STREET: 755 Page Mill Road
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/282,951
FILING DATE: 29-JUL-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: LEHNHARDT, SUSAN K.
REGISTRATION NUMBER: 33,943
REFERENCE/DOCKET NUMBER: 20296-20012.00
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 813-5600
TELEFAX: (415) 494-0792
TELEX: 706141
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 102 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-282-951-2

Query Match 9.7%; Score 37; DB 1; Length 102;
Best Local Similarity 100.0%; Pred. No. 1.8e-28;
Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 345 PNKSGTSGTTRLISGHTCTLTGLTGLTVMGLLT 381
DB 65 PNKSGTSGTTRLISGHTCTLTGLTGLTVMGLLT 101

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OM protein - protein search, using sw model

Run on: February 12, 2003, 11:09:06 ; Search time 35 Seconds
(without alignments)
2242.970 Million cell updates/sec

Title: US-09-623-035-2
Perfect score: 381
Sequence: 1 MVARSPAPALPLGLGLPR.....HTCFTLGLGLTWTGLLT 381

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 671580 seqs, 206047115 residues

Word size: 0

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database: SPTREMBL_21:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp-phage:*
- 10: sp_plant:*
- 11: sp_protent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_rvirus:*
- 16: sp_bacteriap:*
- 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	225	59.1	265	4	Q8TD12
2	197	51.7	419	4	Q8TD11
3	197	51.7	422	4	Q8TD13
4	148	38.8	347	6	Q9MYJ6
5	117	30.7	316	4	Q8TD14
6	99	26.0	305	6	Q9MYJ5
7	99	26.0	347	6	Q9MYJ7
8	35	14.4	55	6	Q18722
9	28	7.3	51	6	Q18724
10	28	7.3	51	6	Q18725
11	24	6.3	343	6	Q9MYJ4
12	24	6.3	343	6	Q9MYJ3
13	22	5.8	271	6	Q9MYJ0
14	22	5.8	278	6	Q9MYJ1
15	22	5.8	343	6	Q9MYJ2
16	22	5.8	343	6	Q9MYJ9

17	15	3.9	63	6	Q18726	atelles geof
18	14	3.7	51	6	Q18723	macaca fusc
19	13	3.4	63	6	Q18727	cebua apell
20	10	2.6	326	6	Q9GLM2	sus scrofa
21	10	2.6	341	6	Q9GLM1	sus scrofa
22	10	2.6	390	11	Q921P0	sus scrofa
23	10	2.6	498	6	Q9GLM0	mus musculus
24	10	2.6	550	12	P88903	kaposi's sa
25	10	2.6	550	12	Q40912	kaposi's sa
26	9	2.4	345	6	Q95LR0	pan troglod
27	9	2.4	2470	13	Q90681	gallus gall
28	8	2.1	185	2	Q9ALJ2	chlorobium
29	8	2.1	202	10	Q9FFZ7	arabidopsis
30	8	2.1	204	10	Q9CAX3	arabidopsis
31	8	2.1	217	2	Q93AG4	azotobacter
32	8	2.1	227	2	Q9AKU1	prosthecoch
33	8	2.1	290	2	Q8VNU7	chlorobium
34	8	2.1	292	2	Q8VNU0	chlorobium
35	8	2.1	292	2	Q8VNU4	prosthecoch
36	8	2.1	324	5	Q44840	caenorhabdl
37	8	2.1	363	6	Q02839	sus scrofa
38	8	2.1	413	16	Q9RZM5	deinococcus
39	8	2.1	426	16	Q8Z526	yersinia pe
40	8	2.1	502	11	Q9ER55	mus musculu
41	8	2.1	533	11	Q08569	cavia porce
42	8	2.1	578	3	Q96V96	orpinomyces
43	8	2.1	732	10	Q94HA5	oryza sativ
44	8	2.1	2967	12	Q41892	hepatitis g
45	8	2.1	11721	4	Q8WX17	homo sapien

ALIGNMENTS

RESULT 1

ID Q8TD12 PRELIMINARY; PRT; 265 AA.
AC Q8TD12;
DT 01-JUN-2002 (TREMBLrel. 21, Created)
DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Decay-accelerating factor 3 (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Hindmarsh E.J., Marks R.M.;
RT "Molecular analysis of human decay-accelerating factor: eight novel
isoforms generated by intron retention and alternative splicing";
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY05759; AAL25834.1; -;
FT NON_TER
SQ SEQUENCE 265 AA; 29370 MW; 3FED6E3F84A79421 CRC64;

Query Match	59.1%	Score 225	DB 4	Length 265
Best local similarity	100.0%	Pred. No. 7e-219		
Matches 225; Conservative	0;	Mismatches	0;	Indels
			0;	Gaps
Oy	130	PGYRREPSLSPKLTCLNLKMSAVFERCKKSCPNPGRIRNGOIDVPGILFGATISFS	189	
Db	1	RGYRREPSLSKLTCLNLKMSAVFERCKKSCPNPGRIRNGOIDVPGILFGATISFS	60	
Oy	190	CNTGYKLFSGTSSFCLLIGSSVQWSDPLPECKREIYCPAPQIDNGIIGERDHYGROSY	249	
Db	61	CNTGYKLFSGTSSFCLLIGSSVQWSDPLPECKREIYCPAPQIDNGIIGERDHYGROSY	120	
Oy	250	TYACKGFTMIGEHISYTCVNNDEGMSGPPRECKGSLTSVPTVYKPTTVNPTTEV	309	
Db	121	TYACKGFTMIGEHISYTCVNNDEGMSGPPRECKGSLTSVPTVYKPTTVNPTTEV	180	
Oy	310	SPTSGKTTTNTTTPNAQATRSPTVSRRTTKHFHETTPNKGSGTSG	354	

Db 181 SPTSOKTTTCTTTPNAQTRSTPVSRTHKHETTPNKGSGTISG 225

RESULT 2

Q8TD11 PRELIMINARY; PRT; 419 AA.

AC 08TD11: 01-JUN-2002 (TReMBLrel. 21, Created)
DT 01-JUN-2002 (TReMBLrel. 21, Last sequence update)
DE 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
Decay-accelerating factor 4ab (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Hindmarsh E.J., Marks R.M.;
RT "Molecular analysis of human decay-accelerating factor: eight novel
isoforms generated by intron retention and alternative splicing."
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY055760; AAL25835.1; -
FT NON_TER 1
SQ SEQUENCE 419 AA; 44796 MW; FACEZE75072A7ESC CRC64;

Query Match 51.7%; Score 197; DB 4; Length 419;
Best local similarity 100.0%; Pred. No. 2.1e-190;
Matches 197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 130 RPYRRRPSISPKLTCLONLKWSTAVFERCKKSCPNPGEIRNGQIDVPGILFGATISFS 189
Db 1 RPYRRRPSISPKLTCLONLKWSTAVFERCKKSCPNPGEIRNGQIDVPGILFGATISFS 60
Qy 190 CMTGYKLFGSTSFCLISGSSVQMSDPLPECREIYCPAPQIDNGIIIGERDHYGRQSV 249
Db 61 CMTGYKLFGSTSFCLISGSSVQMSDPLPECREIYCPAPQIDNGIIIGERDHYGRQSV 120
Qy 250 TYACNKGFTMIGHSIYCTVANNDEGEWGGPPPECRGKSLTSKVPYVOKPTTVVPTTEV 309
Db 121 TYACNKGFTMIGHSIYCTVANNDEGEWGGPPPECRGKSLTSKVPYVOKPTTVVPTTEV 180
Qy 310 SPTSOKTTTCTTTPNAQ 326
Db 181 SPTSOKTTTCTTTPNAQ 197

RESULT 3

Q8TD13 PRELIMINARY; PRT; 422 AA.

AC 08TD13: 01-JUN-2002 (TReMBLrel. 21, Created)
DT 01-JUN-2002 (TReMBLrel. 21, Last sequence update)
DE 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
Decay-accelerating factor 1 ab (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Hindmarsh E.J., Marks R.M.;
RT "Molecular analysis of human decay-accelerating factor: eight novel
isoforms generated by intron retention and alternative splicing."
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY055758; AAL25833.1; -
FT NON_TER 1
SQ SEQUENCE 422 AA; 44849 MW; 7BD89A886CCCD18E CRC64;

Query Match 51.7%; Score 197; DB 4; Length 422;
Best local similarity 100.0%; Pred. No. 2.1e-190;
Matches 197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 130 RPYRRRPSISPKLTCLONLKWSTAVFERCKKSCPNPGEIRNGQIDVPGILFGATISFS 189
Db 1 RPYRRRPSISPKLTCLONLKWSTAVFERCKKSCPNPGEIRNGQIDVPGILFGATISFS 60
Qy 190 CMTGYKLFGSTSFCLISGSSVQMSDPLPECREIYCPAPQIDNGIIIGERDHYGRQSV 249
Db 61 CMTGYKLFGSTSFCLISGSSVQMSDPLPECREIYCPAPQIDNGIIIGERDHYGRQSV 120
Qy 250 TYACNKGFTMIGHSIYCTVANNDEGEWGGPPPECRGKSLTSKVPYVOKPTTVVPTTEV 309
Db 121 TYACNKGFTMIGHSIYCTVANNDEGEWGGPPPECRGKSLTSKVPYVOKPTTVVPTTEV 180
Qy 310 SPTSOKTTTCTTTPNAQ 326
Db 181 SPTSOKTTTCTTTPNAQ 197

RESULT 4

Q9MYJ6 PRELIMINARY; PRT; 347 AA.

AC 09MYJ6: 01-OCT-2000 (TReMBLrel. 15, Created)
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
DE 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
Decay-accelerating factor (Fragment).
OS Pan troglodytes (Chimpanzee).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Pan.
NCBI_TaxID=9598;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=20368351; PubMed=10906393;
RX Kuttner-kondoa L., Baia Subramanian V., Atkinson J.P., Yua J.,
Medofa M.E.;
RT "Conservation in decay accelerating factor (DAF) structure among
primates."
RL Dev. Comp. Immunol. 24:815-827(2000).
DR EMBL; AF149760; AAF73176.1; -
DR HSSP; P08603; IHCC.
DR InterPro; IPR000436; Sush1_SCR_CCP.
DR Pfam; PF00084; sush1_4.
DR SMART; SM00032; CCP; 4.
FT NON_TER 1
SQ SEQUENCE 347 AA; 37872 MW; B03CDAE5DA51BA2 CRC64;

Query Match 38.8%; Score 148; DB 6; Length 347;
Best local similarity 100.0%; Pred. No. 6.1e-141;
Matches 148; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 225 CPAPQIDNGIIIGERDHYGRQSVTYACNKGFTMIGHSIYCTVANNDEGEWGGPPPECR 284
Db 191 CPAPQIDNGIIIGERDHYGRQSVTYACNKGFTMIGHSIYCTVANNDEGEWGGPPPECR 250
Qy 285 GKSLTSKVPYVOKPTTVVPTTEVSPTSOKTTTCTTTPNAQTRSTPVSRTHKHETTP 344
Db 251 GKSLTSKVPYVOKPTTVVPTTEVSPTSOKTTTCTTTPNAQTRSTPVSRTHKHETTP 310
Qy 345 PKNKGSTTSGTTRLLSGHTCFTLGLG 372
Db 311 PKNKGSTTSGTTRLLSGHTCFTLGLG 338

RESULT 5

Q8TD14 PRELIMINARY; PRT; 316 AA.

AC 08TD14: 01-JUN-2002 (TReMBLrel. 21, Created)
DT 01-JUN-2002 (TReMBLrel. 21, Last sequence update)
DE 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
Decay-accelerating factor 1a (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Hindmarsh E.J.; Marks R.M.;
RT "Molecular analysis of human decay-accelerating factor: eight novel
isoforms generated by intron retention and alternative splicing."
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AY055757; AL25832.1; -
FT NON_TER 1
SQ SEQUENCE 316 AA; 33419 MW; DDE6BE563686C778 CRC64;

Query Match 30.7%; Score 117; DB 4; Length 316;
Best Local Similarity 100.0%; Pred. No. 1.2e-109;
Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 210 SVQMSDPLPECRETYCAPPOIDNGIIGERDHYGRQSVTYACNKGKGTMTGHSITYCTV 269
DB 1 SVQMSDPLPECRETYCAPPOIDNGIIGERDHYGRQSVTYACNKGKGTMTGHSITYCTV 60
OY 270 NNDGEMSGPPECRGKSLTSKVPPTVQKPTTVNVPTEVSPTSOKTTTKTTTNAQ 326
DB 61 NNDGEMSGPPECRGKSLTSKVPPTVQKPTTVNVPTEVSPTSOKTTTKTTTNAQ 117

RESULT 6
O9MYJ5 PRELIMINARY; PRT; 305 AA.
AC O9MYJ5;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Decay-accelerating factor (Fragment).
GN CD55
OS Pan troglodytes (Chimpanzee).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Pan.
OX NCBI_TaxID=9598;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20368351; PubMed=10906393;
RA Kuttner-Kondoa L., Bala Subramanian V., Atkinson J.P., Yua J.,
RA Medofa M.E.;
RT "Conservation in decay accelerating factor (DAF) structure among
primates."
RL Dev. Comp. Immunol. 24:815-827(2000).
DR EMBL: AF149761; AAF73177.1; -
DR HSP: P08603; IHCC.
DR InterPro: IPR000436; Sushl_SCR_CCP.
DR Pfam: PF00084; sushl; 4.
DR SMART: SM00032; CCP; 4.
FT NON_TER 1
SQ SEQUENCE 305 AA; 33508 MW; F72A8F398A7C353A CRC64;

Query Match 26.0%; Score 99; DB 6; Length 305;
Best Local Similarity 100.0%; Pred. No. 1.9e-91;
Matches 99; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 42 VPNAOPALEGRTSPEDVTYKCEESVYKIPGKDSYICKGQMSDIEFCNRSCEVP 101
DB 8 VPNAOPALEGRTSPEDVTYKCEESVYKIPGKDSYICKGQMSDIEFCNRSCEVP 67
OY 102 TRLSASLSKOPYTQNTFPVGTVEYECRPGYRREPSLS 140
DB 68 TRLSASLSKOPYTQNTFPVGTVEYECRPGYRREPSLS 106

RESULT 7
O9MYJ7 PRELIMINARY; PRT; 347 AA.
AC O9MYJ7;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)

DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Decay-accelerating factor (Fragment).
GN CD55.
OS Gorilla gorilla (gorilla).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Gorilla.
OX NCBI_TaxID=9593;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20368351; PubMed=10906393;
RA Kuttner-Kondoa L., Bala Subramanian V., Atkinson J.P., Yua J.,
RA Medofa M.E.;
RT "Conservation in decay accelerating factor (DAF) structure among
primates."
RL Dev. Comp. Immunol. 24:815-827(2000).
DR EMBL: AF149759; AAF73175.1; -
DR HSP: P08603; IHFI.
DR InterPro: IPR000436; Sushl_SCR_CCP.
DR Pfam: PF00084; sushl; 4.
DR SMART: SM00032; CCP; 4.
FT NON_TER 1
SQ SEQUENCE 347 AA; 37873 MW; 6DD4AB6C92F89D0 CRC64;

Query Match 26.0%; Score 99; DB 6; Length 347;
Best Local Similarity 100.0%; Pred. No. 2.1e-91;
Matches 99; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 250 TYACKKGFTMTGHSITYCTVNNDEGEMSGPPECRGKSLTSKVPPTVQKPTTVNVPTEV 309
DB 216 TYACKKGFTMTGHSITYCTVNNDEGEMSGPPECRGKSLTSKVPPTVQKPTTVNVPTEV 275
OY 310 SPTSOKTTTKTTTNAQATRSPTVSRTHKHFETPNNG 348
DB 276 SPTSOKTTTKTTTNAQATRSPTVSRTHKHFETPNNG 314

RESULT 8
O18722 PRELIMINARY; PRT; 55 AA.
AC O18722;
DT 01-NOV-1998 (TREMBlrel. 08, Created)
DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)
DT 01-NOV-1998 (TREMBlrel. 08, Last annotation update)
DE Complement decay-accelerating factor (CD55) (Fragment).
GN DAF.
OS Pan troglodytes (Chimpanzee).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Pan.
OX NCBI_TaxID=9598;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Blood;
RX MEDLINE=96099759; PubMed=9435343;
RA Nonaka M., Nonaka M., Takenaka O., Okada N., Okada H.;
RT "A new repetitive sequence uniquely present in the decay-accelerating
factor genes."
RL Immunogenetics 47:246-255(1998).
-1- FUNCTION: PROTECTION OF CELLS FROM COMPLEMENT-MEDIATED DAMAGE (BY
SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE RECEPTORS OF COMPLEMENT ACTIVATION
(RCA) FAMILY.
DR EMBL: AB003313; BAA22901.1; -
KW Complement pathway.
FT NON_TER 1
SQ SEQUENCE 55 AA; 5946 MW; 54FDF4CEE32C1ED9 CRC64;

Query Match 14.4%; Score 55; DB 6; Length 55;
Best Local Similarity 100.0%; Pred. No. 1.3e-47;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 291 KVPPTVQKPTTVNVPTEVSPTSOKTTTKTTTNAQATRSPTVSRTHKHFETTP 345
DB 291 KVPPTVQKPTTVNVPTEVSPTSOKTTTKTTTNAQATRSPTVSRTHKHFETTP 345

Db 1 KVPPTVOKPTTVNPTTEVSPTSOKTTTKTTPNMAQATRSTPVSRITKHFHTTP 55

RESULT 9

ID 018724 PRELIMINARY; PRT; 51 AA.

AC 018724;

DT 01-NOV-1998 (TREMBlrel. 08, Created)

DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)

DE Complement decay-accelerating factor (CD55) (Fragment).

GN DAF.

OS Hylobates syndactylus (Siamaang).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hylobatidae; Hylobates.

OX NCBI_TaxID=9590;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE-BLOOD;

RX MEDLINE=98099759; PubMed=9435343;

RA Nonaka M., Nonaka M., Takenaka O., Okada N., Okada H.;

RT "A new repetitive sequence uniquely present in the decay-accelerating factor genes."

RL Immunogenetics 47:246-255(1998).

CC -1- FUNCTION: PROTECTION OF CELLS FROM COMPLEMENT-MEDIATED DAMAGE (BY SIMILARITY).

CC -1- SIMILARITY: BELONGS TO THE RECEPTORS OF COMPLEMENT ACTIVATION (RCA) FAMILY.

CC EMBL: AB003316; BAA22904.1; -.

DR Complement pathway.

KW NON_TER 1 51

FT SEQUENCE 51 AA; 5514 MW; ED112B05D2A87DC6 CRC64;

SQ

Query Match 7.3%; Score 28; DB 6; Length 51;

Best Local Similarity 100.0%; Pred. No. 2.5e-20;

Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 291 KVPPTVOKPTTVNPTTEVSPTSOKTTT 318

Db 1 KVPPTVOKPTTVNPTTEVSPTSOKTTT 28

RESULT 10

ID 018725 PRELIMINARY; PRT; 51 AA.

AC 018725;

DT 01-NOV-1998 (TREMBlrel. 08, Created)

DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)

DT 01-NOV-1998 (TREMBlrel. 08, Last annotation update)

DE Complement decay-accelerating factor (CD55) (Fragment).

GN DAF.

OS Hylobates lar (Common gibbon).

OC Eukaryota; Metazoa; Chordata; Cranialia; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hylobatidae; Hylobates.

OX NCBI_TaxID=9580;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE-BLOOD;

RX MEDLINE=98099759; PubMed=9435343;

RA Nonaka M., Nonaka M., Takenaka O., Okada N., Okada H.;

RT "A new repetitive sequence uniquely present in the decay-accelerating factor genes."

RL Immunogenetics 47:246-255(1998).

CC -1- FUNCTION: PROTECTION OF CELLS FROM COMPLEMENT-MEDIATED DAMAGE (BY SIMILARITY).

CC -1- SIMILARITY: BELONGS TO THE RECEPTORS OF COMPLEMENT ACTIVATION (RCA) FAMILY.

CC EMBL: AB003317; BAA22905.1; -.

DR Complement pathway.

KW NON_TER 1 51

FT SEQUENCE 51 AA; 5514 MW; ED112B05D2A87DC6 CRC64;

SQ

Query Match 7.3%; Score 28; DB 6; Length 51;

Best Local Similarity 100.0%; Pred. No. 2.5e-20;

Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 291 KVPPTVOKPTTVNPTTEVSPTSOKTTT 318

Db 1 KVPPTVOKPTTVNPTTEVSPTSOKTTT 28

RESULT 11

ID 09MYJ4 PRELIMINARY; PRT; 343 AA.

AC 09MYJ4;

DT 01-OCT-2000 (TREMBlrel. 15, Created)

DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)

DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)

DE Decay-accelerating factor (Fragment).

GN CD55.

OS Papio hamadryas (Hamadryas baboon).

OC Eukaryota; Metazoa; Chordata; Cranialia; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea; Cercopithecidae;

OC Cercopithecoidea; Papio.

OX NCBI_TaxID=9557;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=20368351; PubMed=10906393;

RA Kuttner-Kondoa L., Bala Subramanian V., Atkinson J.P., Yua J., Medofa M.E.;

RT "Conservation in decay accelerating factor (DAF) structure among primates."

RL Dev. Comp. Immunol. 24:815-827(2000).

DR HSSP: P08603; IHFI.

DR InterPro: IPR001969; Aspprotease.site.

DR InterPro: IPR000436; Sushi_SCR_CCP.

DR Pfam: PF00084; sushi; 4.

DR SMART: SM00032; CCP; 4.

DR PROSITE: PS00141; ASP_PROTEASE; UNKNOWN_1.

KW NON_TER 1 1

FT SEQUENCE 343 AA; 37465 MW; 828D47652F68A0C CRC64;

SQ

Query Match 6.3%; Score 24; DB 6; Length 343;

Best Local Similarity 100.0%; Pred. No. 1.4e-15;

Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 217 LPFCREIYCPAPPOINDGIIGER 240

Db 183 LPFCREIYCPAPPOINDGIIGER 206

RESULT 12

ID 09MYJ3 PRELIMINARY; PRT; 343 AA.

AC 09MYJ3;

DT 01-OCT-2000 (TREMBlrel. 15, Created)

DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)

DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)

DE Decay-accelerating factor (Fragment).

GN CD55.

OS Macaca mulatta (Rhesus macaque).

OC Eukaryota; Metazoa; Chordata; Cranialia; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea; Cercopithecidae;

OC Cercopithecoidea; Macaca.

OX NCBI_TaxID=9544;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=20368351; PubMed=10906393;

RA Kuttner-Kondoa L., Bala Subramanian V., Atkinson J.P., Yua J., Medofa M.E.;

RT "Conservation in decay accelerating factor (DAF) structure among primates."

RL Dev. Comp. Immunol. 24:815-827(2000).

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DR EMBL: AF149763; AAF73179.1; -.
DR HSSP: P08603; IHFI.
DR InterPro: IPR000436; Sush1_SCR_CCP.
DR Pfam: PF00084; sush1; 4.
DR SMART: SM00032; CCP; 4.
FT NON_TER 1
SQ SEQUENCE 343 AA; 37296 MW; 2F04847C77316797 CRC64;

Query Match
Best Local Similarity 100.0%; Pred. No. 1.4e-15;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 217 LPECREIYCPAPQIDNGIIGER 240
Db 183 LPECREIYCPAPQIDNGIIGER 206

RESULT 13
Q9MYJ0 PRELIMINARY; PRT; 271 AA.
AC Q9MYJ0;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Decay-accelerating factor (Fragment).
GN CD55.
OS Erythrocebus patas (Red guenon) (Hussar).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecoidea; Erythrocebus.
OX NCBI_TaxID=9538;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN#B289;
RX MEDLINE=20368351; PubMed=10906393;
RA Kuttner-Kondoa L., Bala Subramanian V., Atkinson J.P., Yua J.,
RA Medofa M.E.;
RT "Conservation in decay accelerating factor (DAF) structure among
RT primates.";
RL Dev. Comp. Immunol. 24:815-827(2000).
DR EMBL: AF149766; AAF73182.1; -.
DR HSSP: P08603; IHFI.
DR InterPro: IPR000436; Sush1_SCR_CCP.
DR Pfam: PF00084; sush1; 4.
DR SMART: SM00032; CCP; 4.
FT NON_TER 1
SQ SEQUENCE 271 AA; 29897 MW; 27C36E5CFC3D921 CRC64;

Query Match
Best Local Similarity 100.0%; Pred. No. 1.2e-13;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 217 LPECREIYCPAPQIDNGIIG 238
Db 183 LPECREIYCPAPQIDNGIIG 204

RESULT 14
Q9MYJ1 PRELIMINARY; PRT; 278 AA.
AC Q9MYJ1;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Decay-accelerating factor (Fragment).
GN CD55.
OS Erythrocebus patas (Red guenon) (Hussar).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecoidea; Erythrocebus.
OX NCBI_TaxID=9538;
RN [1]
RP SEQUENCE FROM N.A.
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RC STRAIN#B289;
RX MEDLINE=20368351; PubMed=10906393;
RA Kuttner-Kondoa L., Bala Subramanian V., Atkinson J.P., Yua J.,
RA Medofa M.E.;
RT "Conservation in decay accelerating factor (DAF) structure among
RT primates.";
RL Dev. Comp. Immunol. 24:815-827(2000).
DR EMBL: AF149765; AAF73181.1; -.
DR HSSP: P08603; IHFI.
DR InterPro: IPR000436; Sush1_SCR_CCP.
DR Pfam: PF00084; sush1; 4.
DR SMART: SM00032; CCP; 4.
FT NON_TER 1
SQ SEQUENCE 278 AA; 30607 MW; BF9286DBF703D08F CRC64;

Query Match
Best Local Similarity 100.0%; Pred. No. 1.2e-13;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 217 LPECREIYCPAPQIDNGIIG 238
Db 183 LPECREIYCPAPQIDNGIIG 204

RESULT 15
Q9MYJ2 PRELIMINARY; PRT; 343 AA.
AC Q9MYJ2;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Decay-accelerating factor (Fragment).
GN CD55.
OS Erythrocebus patas (Red guenon) (Hussar).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecoidea; Erythrocebus.
OX NCBI_TaxID=9538;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN#B289;
RX MEDLINE=20368351; PubMed=10906393;
RA Kuttner-Kondoa L., Bala Subramanian V., Atkinson J.P., Yua J.,
RA Medofa M.E.;
RT "Conservation in decay accelerating factor (DAF) structure among
RT primates.";
RL Dev. Comp. Immunol. 24:815-827(2000).
DR EMBL: AF149764; AAF73180.1; -.
DR HSSP: P08603; IHFI.
DR InterPro: IPR000436; Sush1_SCR_CCP.
DR Pfam: PF00084; sush1; 4.
DR SMART: SM00032; CCP; 4.
FT NON_TER 1
SQ SEQUENCE 343 AA; 37423 MW; 6D5DEBDB3DC2112 CRC64;

Query Match
Best Local Similarity 100.0%; Pred. No. 1.4e-13;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 217 LPECREIYCPAPQIDNGIIG 238
Db 183 LPECREIYCPAPQIDNGIIG 204

Search completed: February 12, 2003, 11:11:28
Job time : 37 secs
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